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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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A Geneseq 19Jun03:*

| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
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Gapop 10.0 , Gapext 0.5
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7 188.488 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ህፋ൛危レወט	121	Result
291 291 291 291 291	298	Score
98.0 98.7 95.7 95.7 95.7	98.0	% Query Match
557 577	98.0 57 98.0 57	<pre> Query Match Length DB</pre>
20 113 144 20	35=	DB
AAR28298 AAR41280 AAR33850 AAR39312 AAR39312		ID
Amino acid sequence Sequence encoded b Bacteriocin. Lact Bacteriocin LL-2 p Lactococcal bacter	Nisin precursor pr Pre-nisin A. Lact	Description

5	44	43	42	41	40	9	38	37	36	35	34	ω G	32	31	30	29	28	27	26	25	24	23	22	21	20	19	1.8	17	16	15	14	13	12	11	10
81.5	æ	82	82	92	93	94.5	94.5	94.5	94.5	94.5	96	96	97	97	97	97	104	104	104	104	105	128	157	157	157	157	157	176	178	181	185	185	185	185	185
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AAY31660	AAR85080	AAR30171	AAR41281	AAR39311	AAB11032	AAY03210	AAY43430	AAR37315	AAP98498	ABG72550	AAU75776	AAR50954	AAU75777	AAU75775	AAR95245	AAR28299	AAR95263	AAR56162	AAR43272	AAR37314	AAR50953	AAY31658	ABU59621	AAY91744	20	AAW66445	AAR05237	AAW84352	AAR43070	AAY31659	ABU59619	AAU90978	AAY91742	44	AAR62635
Mutant Lantibiotic	Hyicin M51 (lanthi	locin		Lactococcal bacter	Lactococcus lactis	Amino acid sequenc	S. epidermis readi		Sequence of pre-ep		lac	O	Lactococcus lactis	Lactococcus lactis	La	Sequence of nisin		Sequence of the ba	ū	Epidermin. Staphy	Nisin A/S5A. Lact		cancer -	Cationic peptide S	ld sequen			Peptide QSP-91241	Lactococcus lactis,	Subtilin-nisin chi	Cationic cancer -t	3	Cationic peptide N		Putative intermedi

ALIGNMENTS

RESULT	RESULT 1
ID	AAR05238 standard; protein; 57 AA.
	AAR05238;
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	04-AUG-1990 (first entry)
	Nisin precursor protein and leader peptide encoded by DNA derived from
DE S	Streptococcus lactis ATCC 11454.
	Nisin precursor peptide; nisin leader peptide;
	post-translational modification; Streptococcus lactis ATCC 11454;
	Streptococcus lactis ATCC 11454.
	Key Location/Qualifiers
	tide 123
ij	
	Protein 2457
14	/note="nisin precursor peptide"
\$	
	WO9000558-A.
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	25-JAN-1990.
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	30-JUN-1989; 89WO-US02820.
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Best Local S
Matches 56
immunity. ...
                                                                                                                                                                                                                                                                                                                                                                                                                      -Pre-nisin
 The gene cluster nisABTCIPRK (see AAT29660 and AAT29661) of Lactococcus lactis includes the nisA gene coding for pre-nisin A (AAR95267, see also AAR95263) and the genes for nisin modification, secretion and immunity. nisB (AAR95268) and nisC (AAR95270) are believed to be involved in reactions that modify pre-nisin; nisT (AAR95269) is
                                                                                         Making cell which expresses nisin but gene - by providing cell with variant modification, secretion and immunity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The leader peptide assists in inducing post-translational modification a protein precursor when attached to the precursor as a leader. The precursor polypeptide contains Ser, Thr and Cys which undergo modification after translation to arrive at the the mature protein , having unusual amino acids. Tag a is claimed in the patent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR95267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR95267 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Leader peptide sequence - including post-translational modification of polypeptide(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1990-051685/07.
N-PSDB; AAQ93354.
                                                                    Disclosure; Fig 7; 69pp; English.
                                                                                                                                                                            Dodd HM,
                                                                                                                                                                                                                         19-NOV-1994;
                                                                                                                                                                                                                                               20-NOV-1995;
                                                                                                                                                                                                                                                                       30-MAY-1996
                                                                                                                                                                                                                                                                                           WO9616180-A1
                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                         Key
                                                                                                                                                                                                                                                                                                                                                              Lactococcus lactis strain NIZO R5.
                                                                                                                                                                                                                                                                                                                                                                                              Nisin A; nisA gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 3;
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                                                                                                                                                                                                 (BIOT-) BIOTECHNOLOGY & BIOLOGICAL SCI RES COUNC
                                                                                                                                                                                                                                                                                                                                                                                     lantibiotic;
                                                                                                                                         1996-268616/27.
DB; AAT29660.
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/label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein;
                                                                                                                                                                                                                                                                                                                                                                                    antimicrobial; preservative; antibiotic;
n engineering.
                                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
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98.2%;
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Pred. No. 9.9e
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nisA
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.9e-29;
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RESULT 3
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Best Local S
Matches 56
                                                                                                                                                                                                                                                                                                             nis A gene (see AAX87792). Nisin A is lanthionine-containing bacteriocin. The invention relates to methods of enhancing performance in an animal by administering a bacterium capable of expressing a performance enhancing polypeptide such as misin A or nisin Z. The enhanced performance results in improved growth rates and feed conversion efficiencies. The bacterium, which may be genetically modified to express the performance enhancing polypeptide, is administered to the gastrointestinal tract, especially to an embryo or meonatal animal. If the polypeptide is nisin, it may also inhibit ruminal methane, decrease acetate to propionate ratios and prevent amino acid deamination.

Administration of an appropriate bacterium which may act as a management of the polypeptide is a minimistration of an appropriate bacterium which may act as a management of the polypeptide is a minimistration of an appropriate bacterium which may act as a management of the polypeptide is a minimistration of an appropriate bacterium which may act as a management of the polypeptide is a minimistration of an appropriate bacterium which may act as a management of the polypeptide is a minimistration of an appropriate bacterium which may act as a minimistration of an appropriate bacterium which may act as a minimistration of an appropriate bacterium which may act as a minimistration of an appropriate bacterium which may act as a minimistration of an appropriate bacterium which may act as a minimistration of an appropriate bacterium which may act as a minimistration of an appropriate bacterium which may act as a minimistration of an appropriate bacterium which may act as a minimistration of an appropriate bacterium which may act as a minimistration of an appropriate bacterium which may act as a minimistration of an appropriate bacterium which may act as a minimistration of an appropriate bacterium which may act as a minimistration of an appropriate bacterium which may act as a minimistration of an appropriate bacterium which may act as a minimistra
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel performance enhancing method resulting in improved rates and feed conversion efficiencies in animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nisin A; nis A; lantibiotic; animal performance; growth rate; feed conversion; probiotic; bacteriocin.
                                                                                                                                                            probiotic may also help control enteric pathogens in poultry, polypeptide is produced continuously in the gut, maintaining constant level. The protein is eventually degraded, leaving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 61; 79pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents the nisin A precursor peptide Lactobacillus lactis NIZO R5. The sequence is deduced from the control of the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-FEB-1998;
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DB; AAX87792.
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                                                                                                                     in the meat.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98GB-0003424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 298; DB 17;
Pred. No. 9.9e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A
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Sequence

isolated from L. Lactis NIZO 22186.

food

preservative

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AAR28298;
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ARESULT 4
AAAY03208
ID AAY0
AC AAAY0
AC AAAY0
DT 03-A
XX Subl
KW Gram
XX Subl
KW Gram
XX W099
XX UNKN

 RESULT 5
AAR28298
ID AAR2
XX
AC AAR2
XX
DT 25-M
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Best Local
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Best Local
                                                                                                                                                                                                                                                                                                                                                           This is the amino acid sequence of nicin A used in the method of the invention involving the use of prosublancin 168. The peptide designated sublancin 168, is an antimicrobial useful for treating infections and preserving food against spoilage bacteria, particularly Gram-positive bacteria. Pro-sublancin 168 and pre-sublancin 168, are the precursors of sublancin 168. Sublancin 168 is very stable at low pH and can be autoclaved without damage. It does not decompose after 2 years in aqueous solution of about
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New antimicrobial peptide, sublancin 168, from Bacillus subtilis used for, e.g. treatment of infections caused by Gram negative bacteria and as food preservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hansen JN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-131752/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sublancin 168; antimicrobial; food preservative; Gram-positive bacteria; pre-sublancin 168; nicin
   25-MAR-2003
                                                                       AAR28298 standard;
                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 53; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYMA-) UNIV MARYLAND BALTIMORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9903352-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY03208;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                       56;
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                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                PH
                                                                                                                                                                                  MSTKDFNLDLVSVSKKDSGASPRITSTSLCTPGCKTGALMGCNMKTATCHCSIHVSK 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MSTKDFNLDLVSVSKKDSGASPRITSTSLCTPGCKTGALMGCNMKTATCHCSIHVSK 57
                                                                                                                                                             MSTKDFNLDLVSVSKKDSGASPRITSISLCTPGCKTGALMGCNMKTATCHCSIHVSK 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MSTKDFNLDLVSVSKKDSGASPRITSISLCTPGCKTGALMGCNMKTATCHCSIHVSK 57
                                                                                                                                                                                                                                                                                                            57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence of nicin
                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98.0%;
ilarity 98.2%;
Conservative
(updated)
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                                                                       Protein;
                                                                                                                                                                                                                                                    98.0%;
                                                                       57
                                                                                                                                                                                                                                   0;
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                                                                                                                                                                                                                                   Score 298; DB 20;
Pred. No. 9.9e-29;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 298; DB 20;
Pred. No. 9.9e-29;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                       Length 57;
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                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                   Gaps
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ARBSULT 6
ARACATION
ID AARRA
XX AARRA
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DT 25-M
DT 10-M
XX
XX Bact
XX Bact
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XX inhi
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                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                Lactococcus lactis
                                                                                                       Bacteriocin
                                                                                                                                           25-MAR-2003
10-MAR-1994
                                                                                                                                                                                               AAR41280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Кeу
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence encoded by nisz gene
                                                    Bacteriocin;
inhibit.
                                                                                                                                                                                                                                   AAR41280 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1992-382116/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                De Vos WM, Kuipers OP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-APR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9218633-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lactococcus lactis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lantibiotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                    rocal
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                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 AA;
                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nisin Z;
                                                                   LL-2; gram
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                         (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92WO-NL00068
                                                                                                                                                                                                                                   Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                    95.7%;
96.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nisin A; analogue;
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Total DNA was isolated from the L. lactis strains NIZO 22186 and NIZO R5. With the aid of the nisA gene of strain NIZO R5 as a probe, a 4.5 kb HindIII fragment was identified in the total DNA strain NIZO 22186, which was then cloned in M13 mpl8. The DNA sequence of the gene for nisin Z production (nisZ) was determined by making use of oligos complementary to the 5' and 3' flanking sequences of the nisA gene. The nucleotide sequence for the nisA gene is found to be identical to that of the nisA gene with the exception of a C to A transversion in posn. 148 which results in the replacement of AA His27 by Asn27. The above indicate that the structure of nisin Z is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New lantiobiotic cpds. related to nisin {\bf A} - and Lactococcus strains which produce them, useful as preservatives for foods and animal feeds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example; Fig 3; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NIZO-) NIZO STICHTING NEDERLANDS INST ZUIVELOND
                                                                                                                                                                                                                                                                                                                                                                                                             in AAR28299.
on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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positive
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                                                                                                                                                                                                                                                               57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 291; DB 1: Pred. No. 7e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
   bacteria; antimicrobial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
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                  8
                                                                                   Query Match
Best Local S
Matches 55
                                                                                                                         encoded protein inhibits selected gram positive bacteria and this property is enhanced if further purified by HPLC. The materials being treated to provide inhibition are preferably foods, although other materials may be treated.
                                                                                                                                              The sequence (AAQ49150) was amplified using primers (AAQ49151-52). encoded protein inhibits selected gram positive bacteria and this property is enhanced if further purified by HPLC. The materials
                                                                                                                                                                                                                                                                                                                                                                                             US5232849-A.
                                                                                  Sequence
                                                                                                                                                                                       Disclosure; Page 13-14 (col 15,16,17,18); 14pp; English
                                                                                                                                                                                                           Bacteriocin from Lactococcus lactis subspecies lactis - inhibitory against Gram-positive bacteria
                                                                                                                                                                                                                                            WPI; 1993-287077/36.
N-PSDB; AAQ49150.
                                                                                                                                                                                                                                                                          Henderson JT,
                                                                                                                                                                                                                                                                                                                    01-JUL-1991;
14-MAY-1992;
                                                                                                                                                                                                                                                                                                                                                    14-MAY-1992;
                                                                                                                                                                                                                                                                                                                                                                         03-AUG-1993
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                                                                                                                                                                                                                                                                                                (UNIL ) QUEST
                                                                                                       (Updated
                                         55
                                                   Similarity
            MSTKDFNLDLVSVSKKDSGASPRITSTSLCTPGCKTGALMGCNMKTATCHCSIHVSK 57
                                                                                                     on 25-MAR-2003
on 25-MAR-2003
MSTKDFNLDLVSVSKKDSGASPRITSISLCTPGCKTGALMGCNMKTATCNCSIHVSK 57
                                                                                  57
                                         Conservative
                                                                                  A.
                                                                                                                                                                                                                                                                                               INT FLAVORS & FOOD INGREDIENTS CO
                                                                                                                                                                                                                                                                          Marugg
                                                                                                                                                                                                                                                                                                                    91US-0721774
92US-0882079
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/note=
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/note=
                                                                                                                                                                                                                                                                                                                                                                                                                          52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= sig_peptide
24..57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= mat_protein
/note= "Claim 3"
                                                                                                                                                                                                                                                                                                                                                                                                                  note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       notes
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                                                  95.7%;
                                                                                                                                                                                                                                                                          'n,
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                                                                                                                                                                                                                                                                                                                                                                                                                                     "The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The CH2 in the side chain joins the S in residue 30"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The CH2 in the side chain joins the S in residue 34"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The S joins the side chain of residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The S joins the side chain of residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The S joins the side chain of residue
                                                                                                      t t
                                                                                                                                                                                                                                                                                                                                                                                                                  "The S joins the side chain of residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The S joins the side chain of residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the
                                                                                                      correct PF field.)
                                                                                                                                                                                                                                                                           Van WASSENAAR PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CH2 in the side chain joins
S in residue 51"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CH2 in the side chain joins S in residue 42"
                                                                                                                                                                                                                                                                                                                                                                                                                                    CH2 in the side chain joins
S in residue 52"
                                       Score 291; DB 14;
Pred. No. 7e-28;
1; Mismatches 1;
                                        1.
                                                                                                                                                                                                                                                                          Vedamuthu
                                                            Length
                                         Indels
                                                                                                                                                                                                                         useful
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                                                                                                                                                                                                                         88
                                        Gaps
                                                                                                                                                                      The
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RESULT 7

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RESULT 8
AAR39312
ID AAR3
XX
AC AAR3
AC AAR3
DT 25-M
DT 21-J
XX
XX
XX
XX
AX
DE Lact
XX
XX
XX
XX
XX
XX
XX
OS Lact
XX
OS Lact
                                                                                                                                                                                     밁
                                                                                                                                                                                                       S
                                                                                                                                                                                                                               Query Match
Best Local S
Matches 55
                                                                                                                                                                                                                                                                                                                  The sequence is that of bacteriocin LL-2 precursor which can be used in a method for the inhibition of Gram-positive bacteria. LL-2 is especially useful for treatment of food, although other non-food materials may also be treated.
         Lactococcus lactis (subspecies lactis)
                                Bacteriocin;
                                                                         25-MAR-2003
21-JAN-1994
                                                                                                          AAR39312;
                                                                                                                                AAR39312 standard; Protein;
                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 13; 14pp; English.
                                                                                                                                                                                                                                                                                                                                                                                             Inhibition of Gram-positive bacteria - using bacteriocin derived from Lactococcus lactis sub-species lactis NRRL B-18809
                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1993-017533/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vedamuthu ER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUL-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUL-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lactococcus lactis sub-species lactis NRRL B-18809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Food treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteriocin LL-2 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAR-2003
12-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR33850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR33850 standard; Protein; 57
                                                     Lactococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US5173297-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UNIL ) QUEST
                                                                                                                                                                                                                                55;
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                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                              on 25-MAR-2003 to correct
on 25-MAR-2003 to correct
                                                                                                                                                                                      MSTKDFNLDLVSVSKKDSGASPRITSISLCTPGCKTGALMGCNMKTATCNCSIHVSK
                                                                                                                                                                                                  MSTKDFNLDLVSVSKKDSGASPRITSTSLCTPGCKTGALMGCNMKTATCHCSIHVSK 57
                                                                                                                                                                                                                                                                         57 AA;
                                                                                                                                                                                                                               95.7%;
ilarity 96.5%;
Conservative
                                                    bacteriocin polypeptide precursor
                                                                         (updated)
(first ent
                              inhibition; polypeptide; Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INT FLAVORS & FOOD INGREDIENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Henderson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91US-0721774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91US-0721774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*note= "signal peptide"
24..57
/*note= "mature peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                          entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŢŢ,
                                                                                                                                 57
                                                                                                                                                                                                                               Score 291; DB 14;
Pred. No. 7e-28;
1; Mismatches 1.
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                                                                                                                                 B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                               PA field.)
PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vanwassenaar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ႘
                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                    Length 57
                                                                                                                                                                                                                                Indels
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RESULT 9
AAY06670
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Best Local S
Matches 55
                                                                                                                                                                                                                                                                                                                                                                                                 The isolated bactriocin obtained from the polypeptide precursor has an inhibitory activity against selected Gram positive bacteria. The amount of bacteriocin required to provide inhibition is 15-100 arbitrary units per gram of material. The materials being treated with the bacteriocin to provide inhibition are especially foodstuff (Updated on 25-MAR-2003 to correct Pf field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated and purified polypeptide from Lactococcus lactis sub species lactis - has inhibitory activity against gram-positive bacteria for e.g. food etc.
                           (PFIZ )
                                                                                                26-AUG-1999
                                                                                                                                                                  Nisin Z;
                                                                                                                                                                                      Nisin Z of Lactobacillus lactis.
                                                                                                                                                                                                          09-NOV-1999
                                                                                                                                                                                                                             AAY06670;
                                                                                                                                                                                                                                                AAY06670 standard;
                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Column 17-18; 13pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Henderson JT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1991;
14-MAY-1992;
        Flanagan AJ,
                                                         18-FEB-1998;
                                                                                                                    WO9941978-A1.
                                                                                                                                      Lactobacillus
                                                                                                                                                         feed conversion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-MAY-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US5231165-A
                                                                           12-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UNIL ) QUEST
                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                           PFIZER :
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                                                                                                                                                                  nis Z;
                                                                                                                                                                                                                                                                                                  MSTKDFNLDLVSVSKKDSGASPRITSISLCTPGCKTGALMGCNMKTATCNCSIHVSK 57
                                                                                                                                                                                                                                                                                                                                                                                 57
                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INT FLAVORS & FOOD INGREDIENTS CO
        Haxell
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                                                          98GB-0003424
                                                                            99WO-IB00250
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92US-0882715.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92US-0882715
                                                                                                                                                                 lantibiotic; animal performance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24..57
/label= Bacteriocin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                         bacteriocin;
                                                                                                                                                                                                                                                 Protein; 57
                                                                                                                                                                                                                                                                                                                                                  95.7%;
96.5%;
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        Rolph
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                                                                                                                                                                                                                                                                                                                                                  Score 291; DB 14;
Pred. No. 7e-28;
                                                                                                                                                        probiotic
                                                                                                                                                                                                                                                 A
                                                                                                                                                                                                                                                                                                                                         Mismatches
         TP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vedamuthu
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                                                                                                                                                                 growth
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ARESULT 10
AAR62635
ID AAR62635
AC AAR62
XX AAR62
XX Inth
XX I
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         enhancing polypeptide such as nisin A or nisin Z. The enhanced performance results in improved growth rates and feed conversion efficiencies. The bacterium, which may be genetically modified to express the performance enhancing polypeptide, is administered to the gastrointestinal tract, especially to an embryo or neonatal animal. If the polypeptide is nisin, it may also inhibit ruminal methane, decrease acetate to propionate ratios and prevent amino acid deamination. Administration of an appropriate bacterium which may act as a probiotic may also help control enteric pathogens in poultry. The polypeptide is produced continuously in the gut, maintaining a constant level. The protein is eventually degraded, leaving no residues in the meat.
                                                                                                                                                                                                                                                                                                           Prepn. of lanthionine contg. peptide(s) antiviral drugs, immunosuppressants and
                                                                                                                                                                                                                    Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-SEP-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JP06253885-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Putative intermediate for lanthionine-contg. peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR62635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR62635 standard; peptide; 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                relates to methods of enhancing performance in an animal by administrating a bacterium capable of expression. The enhance of expression of the enhance of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents the nisin Z peptide of Lactobacillus lactis strain 22186. Nisin Z is a natural analogue of nisin A AAY06665), a lanthionine-containing bacteriocin. The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 71; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel performance enhancing method resulting in improved growth rates and feed conversion efficiencies in animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AJIN ) AJINOMOTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunosuppressant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lanthionine; methyllanthionine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1999-527402/44.
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                                                                                                                                                                                                                2; Page 7; 8pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MSTKDFNLDLVSVSKKDSGASPRITSISLCTPGCKTGALMGCNMKTATCNCSIHVSK 57
                                                                                                                                                                                                                                                                                                      drugs, immunosuppressants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93JP-0048385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antimicrobial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95.7%;
96.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 291; DB 2
Pred. No. 7e-28;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lantibiotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           enzyme

    useful as antimicrobial,
enzyme inhibitors

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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0,

This is one of 5 peptides (AAR62635-R63639) containing Cys and Thr residues which were synthesised and tested for their useful as intermediates for the preparation of peptides which include lanthionine. Peptides 3 and 4 (AAR62637-8) produced lanthionine

produced lanthionine,

usefulness

Ser or

methyllanthionine could be produced from peptide

밁

ITSISLCTPGCKTGALMGCNMKTATCHCSIHVSK 34

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RESULT 11
AAW6643
ID AAW66
ACC AAW66
ACC AAW66
ACC AAW66
ACC AAW66
ACC ACTIO
XX Indol
KW bacte
XX INGOL
KW BACTE
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KW INGOL
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Best Local S
Matches 33
                                                                                                                                      Query Match
                                                                                      Matches
                                                                                                                                                                                                                                      AAW66393 to AAW66469 represent native cationic peptides from the present invention. The present invention describes compositions and methods for treating infection, especially bacterial infections. The compositions and methods use cationic peptides in combination with an antibiotic agent which are then administered to a patient to enhance the activity of the antibiotic agent, to overcome: (a) tolerance; (b) acquired resistance; and (c) inherent resistance. The combinations of antibiotics and cationic peptides can provide synergistic activity against a microorganism that is tolerant, inherently resistant, or has acquired resistance to an antibiotic agent. They can be used for killing e.g. bacteria, fungi, parasites and viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            both lanthionine and 2 (AAR62636).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New indolicidin peptide analogues - useful for, e.g. enhancing activity of antibiotic or overcoming tolerance, acquired resistance or inherent resistance of microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fraser JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-FEB-1998;
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                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 10; 105pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-SEP-1997;
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20-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lactococcus lactis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bacteria; fungus; parasite; virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indolicidin analogue; resistance; cationic peptide; antibiotic;
bacterial infection; tolerance; antibacterial; microorganism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-JAN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MICR-) MICROLOGIX BIOTECH INC
                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 ITSTSLCTPGCKTGALMGCNMKTATCHCSIHVSK 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33;
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                                                                                                                Similarity
ITSTSLCTPGCKTGALMGCNMKTATCHCSIHVSK 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ITSISLCTPGCKTGALMGCNMKTATCHCSIHVSK 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 AA;
                                                                                                                                                                                              34 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                McNicol PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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97US-0040649.
97US-0915314.
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                                                                                                             60.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60.9%;
97.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   West MHP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English.
                                                                                    <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 185;
Pred. No. 2
                                                                                                                Score 185; DB 19;
Pred. No. 2.8e-15;
                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 15;
.8e-15;
                                                                                                                                      Length 34;
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                                                                                    Indels
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                                                                                    Gaps
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ARESULT 12
ARAY91742
ID ARAY91742
XX ARY91742
AC ARAY917
AC ARAY917
AC ARAY91
AC ARAY91
AC ARAY91
AC ARAY91
AC ARAY91
AC ARAY91
AC CALic
XX Catic
XX Catic
XX Catic
XX Isuka
X
  RESULT 13
AAU90978
ID AAU90
XX.
AC AAU90
XX O5-JU
DT 05-JU
XX
XX
Trans
XX Trans
KW Cell
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Best Local S
Matches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents a cationic peptide amino acid sequence, which can be used in the pharmaceutical composition of the invention. The invention relates to a pharmaceutical composition containing at least one activated polyoxyalkylene (APO) modified actionic peptide. The modification of peptides with APO increases their activity against tumour cells, including those with a multidrug resistant phenotype. The pharmaceutical composition can be used to treat tumours; specifically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cationic peptide; tumour; pharmaceutical composition; cancer; treatment; leukaemia; polyoxyalkylene-modified; APO; lymphoma; multiple myeloma; breast; lung; ovary; cervix; uterus; skin; prostate; liver; colon; multidrug resistance.
Transplant; antimicrobial peptide; pore forming agent; cell surface receptor binding compound; kidney transplant;
                                                                                                                                             05-JUN-2002
                                                                                                                                                                                                    AAU90978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel pharmaceutical composition containing optionally activated polyoxyalkylene-modified cationic peptides, useful for treating tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-223549/19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cationic peptide Nisin amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-JUN-2000
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                                                                                   Transplant media associated antimicrobial peptide #14.
                                                                                                                                                                                                                                                        AAU90978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 11; 94pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Friedland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lymphoma, leukaemiā, multiple myeloma, or tumours of breast, lung, ovary,
servix, uterus, skin, prostate, liver and colon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                        standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                standard; Peptide; 34
                                                                                                                                                                                                                                                                                                                                                                                                ITSISLCTPGCKTGALMGCNMKTATCHCSIHVSK 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ä,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                             (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Krieger
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                                                                                                                                                                                                                                                        Peptide;
                                                                                                                                             entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 185; DB 21;
Pred. No. 2.8e-15;
0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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Lactococcus lactis.

cardioplegia; organ transplant; transplant rejection.

京大 子二年五月

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RESULT 14
ABU59619
ID ABU59
XX ABU59
XX ABU59
XX CATic
XX CATic
XX Targe
KW Targe
KW Cathe
KW Targe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cc antimicrobial polypeptides or pore forming agents and/or cell surface cc receptor binding compounds. The media is capable of extending the preservation period past 72 hours and can provide organs with increased cc functionality upon transplant animals receiving kidneys stored in the media of the present invention for either three or four days had serum creatinine levels of less than half of those observed in control animals cc receiving kidneys stored in UW solution (defined in the specification) and a more preferable prognosis for the transplant patient. The media of the invention are useful for decreasing the incidence and/or severity of delayed graft function in patients receiving transplanted kidneys stored cc and/or treated in the media. The media may also be used in procedures cc such as cardioplegia. It is contemplated that transplant of healthier corporate leads to a decrease in chronic rejection. This sequence represents an animicrobial peptide studied in the development of the transplant
                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local
                                                                                     Targeting ligand; bioactive agent; polymer matrix; cancer; cytostatic; cathepsin-D substrate; peptides; neuroreceptor; adrenal receptor; fibronectin; vitronectin; integrin; RGD motif; angiogenic endothelium;
                                                                                                                                                            Cationic cancer -targeting peptide #51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Media comprising antimicrobial polypeptides or pore forming agents and/or cell surface receptor binding compounds useful for the storage and preservation of organs prior to transplant -
US2002041898-A1
                                                                                                                                                                                                    22-APR-2003
                                                                                                                                                                                                                                        ABU59619;
                                                                                                                                                                                                                                                                        ABU59619 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention antimicrobial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 25; 78pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-JUL-2000; 2000US-221632P
17-NOV-2000; 2000US-249602P
15-MAY-2001; 2001US-290932P
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                                                                    tumour; cationic
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33; Conserv
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nilarity 97.1%;
Conservative
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                                                                    cancer-targeting peptide.
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RESULT 15
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Best Local :
                                                                                    Chimeric
Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     substrate peptides, peptides targeting receptors in the brain and kidney, peptides recognising fibronectin- and vitronectin-binding integrins, peptides targeting the RGD (Arg-Gly-Rsp)-motif in, e.g., antibodies, peptides targeting the angiogenic endothelium of solid tumours, tissue specific peptides (e.g. of lung, skin, pancreas, intestine, uterus, adrenal gland and retina), and cationic cancertargeting peptides. The present sequence is a peptide targeting ligand disclosed in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          homogeneously dispersed in a targeted matrix (polymer and targeting ligand). Also included are a targeted matrix for use as a delivery vehicle comprising a polymer associated with a targeting ligand, enhancing the bicavailability of an agent comprising administration of the composition and treating cancer comprising administration of novel composition. The method is useful for targeted delivery of a despecially in cancer therapy. The targeting ligand may be a peptide. Examples of targeting peptides are disclosed including cathepsin-D
                                                                                                                                                                          Subtilin-nisin chimera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
             Protein
                                        Peptide
                                                                                                                                 preservative.
                                                                                                                                                Nisin;
                                                                                                                                                                                                         09-NOV-1999
                                                                                                                                                                                                                                      AAY31659;
                                                                                                                                                                                                                                                                  AAY31659 standard; Protein; 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a composition comprising a bioactive agent homogeneously dispersed in a targeted matrix (polymer and targeting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page14; 46pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Targeted delivery system comprising a bioactive agent homogeneously dispersed in a targeted matrix is especially useful in cancer therapy
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31-OCT-2000;
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(MATS/) MATSUNAGA T O.
(RAMA/) RAMASWAMI V.
(ROMA/) ROMANOWSKI M J.
                                                                                                                                                                                                                                                                                                                                                           24 ITSTSLCTPGCKTGALMGCNMKTATCHCSIHVSK 57
                                                                                                                                            subtilin;
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                                                                                    Lactococcus lactis. Bacillus subtilis.
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2000US-0703474.
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                                                                                                                                                                                                      (first entry)
                                                     Location/Qualifiers
                          /note= "signal peptide"
                                                                                                                                               lantibiotic; chimera; mutant; bacteriocide;
'note= "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                 60.9%;
97.1%;
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Pred. No. 2.8e-15;
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The present sequence represents a chimeric pre-peptide composed of a subtilin leader region and a subtilin-nisin fusion comprising residues 1-11 of Bacillus subtilis subtilin and residues 12-32 of Lactococcus lactis nisin. The subtilin-nisin fusion was not processed into a functional lantibiotic when expressed in B. subtilis. A heterogeneous mixture of products was produced, with none of the products having the expected properties of a correctly processed polypeptide. However, the mixture contained a minor component with a specific activity that exceeded that of nisin. The invention provides lantibiotic mutants and chimeras (see also AAV31658) having enhanced activity and stability compared to nisin and subtilin. They can be produced by cultivation of transformed host cells and used e.g. as food preservatives to treat, kill or inhibit the growth of microorganisms and/or their spores.
                                                                                  Query Match
Best Local Similarity
Matches 33; Conserv
                                                                                                                                                                  Sequence
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N-PSDB; AAX87829.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lantibiotic mutants and chimera(s) - having enhanced stability and activity compared to nisin
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41 AA;
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/note= "nisin (1-11)"
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                                                                                  59.5%; Score 181; DB 18; Length 41; 80.5%; Pred. No. 1.1e-14; tive 2; Mismatches 6; Indels
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Search completed: January 12, 2004, 14:24:21 Job time : 49 secs

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Result
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Listing first 45 summaries
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Perfect score:
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US-08-836-687B-26
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US-08-836-687B-44
US-08-836-687B-47
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US-08-930-619-206
US-08-930-619-206
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US-08-935-494-9
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US-08-220-033-7
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                                                      Sequence 28, Application US/08836687B Patent No. 6448034 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: PRODUCTION OF VARIANT NISIN FILE REFERENCE: 20747/70
CURRENT APPLICATION NUMBER: US/08/836,687B
CURRENT FILING DATE: 1995-11-20
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 26
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CURRENT APPLICATION NUMBER: US/08/836,687B
CURRENT FILING DATE: 1995-11-20
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 24
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Best Local Similarity
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Patent No. 6448034
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APPLICANT: Gasson, Michael John
APPLICANT: Dodd, Helen Mair
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Patent No. 644803
APPLICANT: Gasson, Michael John
APPLICANT: Dodd, Helen Mair
TITLE OF INVENTION: PRODUCTION OF VARIANT NISIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Gasson, Michael John
APPLICANT: Dodd, Helen Mair
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                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Lactococcus sp.
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ORGANISM: Lactococcus
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96.5%;
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96.5%;
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                                                                                                                                                                                                                                                             Score 295; DB 4; Length 57; Pred. No. 4.1e-29; Indels
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Pred. No. 4.1e-29;
1; Mismatches 1
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2,
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                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NL 9100634
FILING DATE: 11-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/NL92/00068
FILING DATE: 09-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, ANDREW J.
REGISTRATION NUMBER: 32,925
REFERENCE/DOCKET NUMBER: BO 37078
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CURRENT FILING DATE: 1995-11-20
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                          TELEFAX: 703/685-0573
TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TYPE: PRT
ORGANISM: Lactococcus
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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APPLICANT:
APPLICANT:
                                                                      TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/129,15;
FILING DATE: 07-OCT-1993
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                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                   TELEPHONE: 703/685-0573
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                          LENGTH:
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                                                                                                                            57 amino acids
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745 South 23rd Street, Second Floor
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                                                                                          linear
                                                                                                                                                                                                                   703/521-2297
                                                                      protein
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94.7%;
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95.7%;
96.5%;
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ACID BACTERIA WHICH PRODUCE SUCH LANTIBIOTICS, METHOD
CONSTRUCTING SUCH LACTIC ACID BACTERIA AND METHOD FOR
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Pred. No. 9.6e-29;
Score 291; DB 1;
Pred. No. 1.3e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Version #1.25
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RESULT 8
US-08-836-687B-40
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                                                                                                                                                    Query Match 95.7%;
Best Local Similarity 96.5%;
Matches 55; Conservative
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TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 57 amino acids
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APPLICATION NUMBER: NL 9:
FILING DATE: 11-APR-1991
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEPHONE: 703/521-2297
TELEFAX: 703/685-0573
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CURRENT APPLICATION DATA:
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FILING DATE: 09-APR-1992
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 32,925
REFERENCE/DOCKET NUMBER: BO
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FILING DATE: 07-OCT-1993
CLASSIFICATION: 435
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                                                                                              1 MSTKDENLDLVSVSKKDSGASPRITSTSLCTPGCKTGALMGCNMKTATCHCSIHVSK 57
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745 South 23rd Street, Second Floor
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KUIPERS, Oscar P.
                                                                                                                                                                                                                                                                      linear
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                                                                                                                                                                      Score 291; DB 2;
Pred. No. 1.3e-28;
                                                                                                                                                  Mismatches
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                                                                                                                                                                                      Length 57;
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US-08-836-687B-43
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                                                     TITLE OF INVENTION: PRODUCTION OF VARIANT NISIN FILE REFERENCE: 20747/70 CURRENT APPLICATION NUMBER: US/08/836,687B CURRENT FILING DATE: 1995-11-20 NUMBER OF SEQ ID NOS: 51 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 42
                                                                                                                                                                                                                          Patent No. 6448034
GENERAL INFORMATION:
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Matches
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 43
LENGTH: 57
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APPLICANT: Dodd, Helen Mair
TITLE OF INVENTION: PRODUCTION OF VARIANT NISIN
FILE REFERENCE: 20747/70
CURRENT APPLICATION NUMBER: US/08/836,687B
CURRENT FILING DATE: 1995-11-20
NUMBER OF SEQ ID NOS: 51
SOPTWARE: Patentin Ver. 2.1
SEQ ID NO 40
                                                                                                                                                                                                                                                Sequence 42, Application US/08836687B Patent No. 6448034
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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CURRENT APPLICATION NUMBER: US/08/836,687B
CURRENT FILING DATE: 1995-11-20
                                                                                                                                                                                       APPLICANT: Gasson, Michael John APPLICANT: Dodd, Helen Mair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Gasson, Michael Jo APPLICANT: Dodd, Helen Mair
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ORGANISM: Lactococcus sp
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                       TYPE: PRT
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96.5%;
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96.5%;
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Pred. No. 1.3e-28;
0; Mismatches 2
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Pred. No. 1.3e-28;
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RESULT 13
US-08-836-687B-45
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US-08-836-687B-46
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CURRENT APPLICATION NUMBER: US/08/836,687B
CURRENT FILING DATE: 1995-11-20
NUMBER OF SEQ ID NOS: 51
SOPTWARE: Patentin Ver. 2.1
SEQ ID NO 46
LENGTH: 57
                GENERAL INFORMATION:
APPLICANT: Gasson, Michael John
APPLICANT: Dodd, Helen Mair
                                                                   Sequence 45, Application US/08836687B Patent No. 6448034
                                                                                                                                                                                                                                                                        Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 44, Applical Patent No. 6448034 GENERAL INFORMATION:
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APPLICANT: Gasson, Michael John
APPLICANT: Dodd, Helen Mair
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                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 20747/70
CURRENT APPLICATION NUMBER: US/08/836,687B
CURRENT FILING DATE: 1995-11-20
NUMBER OF SEQ ID NOS: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gasson, Michael John
APPLICANT: Dodd, Helen Mair
TITLE OF INVENTION: PRODUCTION OF VARIANT NISIN
TITLE OF INVENTION: PRODUCTION OF VARIANT NISIN
                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Lactococcus sp.
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o. 6448034
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Pred. No. 2.2e
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Pred. No. 2
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RESULT 14
US-08-773-731A-2
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CURRENT APPLICATION NUMBER: US/08/836,687B
CURRENT FILING DATE: 1995-11-20
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Appric
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                               Query Match
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Best Local Similarity 94.7%;
                                                                                                                                                                    TELEFAX: 202-887-0689
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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TYPE: PRT
ORGANISM: Lactococcus sp.
                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 83 amino acids
                                                                                                                                                                                                                                                                                    FILING DATE: 02-APR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 18-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/
FILING DATE: 01-APR-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: NISINS
                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                        TELEPHONE: 202-887-0689
                                                                                                                                                                                                                                      NAME: Brady, Jr., James W.
REGISTRATION NUMBER: 32,115
REFERENCE/DOCKET NUMBER: E8280.016/P016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 2101 L St
CITY: Washington
                                                                                                   TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: GB 9207267.7
               Local Similarity
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2101 L Street N.W.
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SYSTEM: PC-DOS/MS-DOS
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94.7%;
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Score 285; DB 3; Length 83; Pred. No. 1e-27; 0; Mismatches 3; Indels
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Pred. No. 6.8e-28;
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                             Score
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT NEW PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US07_NEW PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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/Ggn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
/Ggn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
/Ggn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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                                                                                                      6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
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6/ptodata/1/pubpaa/US08 PUBCOMB.pep:*
                                                                                                                                                                                 US-09-030-619-206
US-09-917-340-14
2 US-10-277-233-206
US-09-030-619-208
US-10-372-098-9
US-10-082-618-4
US-10-277-233-208
US-10-372-098-10
US-10-082-618-6
US-10-082-618-1
US-10-184-644-211
US-10-184-634-211
US-10-140-472-67
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                Sequence 206, App
Sequence 14, Appl
Sequence 208, App
Sequence 9, Appli
Sequence 9, Appli
Sequence 208, App
Sequence 10, Appli
Sequence 10, Appli
Sequence 1, Appli
Sequence 11, Appli
Sequence 211, App
Sequence 211, App
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16
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0-184-644-1	-10-063-685-3	0-146-731-	-10-123-155-3	-10-141-759-3	-10-141-756-3	-10-140-923-	40-86	-10-140-805-3	-10-137-871-	0-158-790-3	-10-142-885-31	0-141-761-	-10-140-472-	0-184-634-23	2	-10-063-685-	-10-184-634-	44-33	0	-10-123-155-6	-10-141-759-	0-141-756-6	-10-140-923-	0-140-864-	-10-140-805-	0-137-871-	-10-158-790-6	0-142-885-	-10-141-761-
e 147,	equence 31,	e 317,	e 317,	e 317,	e 317,	e 317,	e 317,	e 317,	e 317,	e 317,	e 317,	e 317,	e 317,	e 235,	e 235,	e 61,	e 335,	e 335,	e 67,	e 67,	e 67,	e 67,	Sequence 67, Appl	e 67,	e 67,	e 67,	e 67,	e 67,	•

ALIGNMENTS

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RESULT 2
US-10-372-098-8
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                  Sequence 8, Application US/10372098

Publication No. US20030166835A1

GENERAL INFORMATION:

APPLICANT: UNIVERSITY OF MARYLAND

TITLE OF INVENTION: SUBLANCIN LANTIBIOTIC PRODUCED BY BACILLUS SUBTILIS 168

FILE REFERENCE: 8172-8072
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US-10-082-618-5
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Publication No. US20030175207A1
GENERAL INFORMATION:
APPLICANT: OLSTEIN, ALAN D.
APPLICANT: FEIRTAG, JOELLEN
TITLE OF INVENTION: BACTERIOCIN-METAL COMPLEXES IN THE DETECTION OF TITLE OF INVENTION: PATHOCSNS AND OTHER BIOLOGICAL ANALYTES
FILE REFERENCE: 7005-0003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/082,618
CURRENT FILING DATE: 2002-02-22
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 57
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CURRENT APPLICATION NUMBER: US/10/372,098
                                                                                                                                                                                                                                                                                                                                                    Local
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US-09-917-340-14

Sequence 14, Application US/09917340
Patent No. US20020090369A1
GENERAL INFORMATION:
APPLICANT: Murphy, Christopher J.
APPLICANT: McAnulty, Jonathan F.
APPLICANT: Reid, Ted W.
TITLE OF INVENTION: Transplant Media
FILE REFERENCE: TPLANT-06468
CURRENT APPLICATION NUMBER: US/09/917,340
CURRENT APPLICATION NUMBER: 60/221,632
PRIOR APPLICATION NUMBER: 60/221,632
PRIOR FILING DATE: 2000-07-28
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; SEQ ID NO 8
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
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US-09-030-619-206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Fraser, Janet R.
APPLICANT: West, Michael H.P.
APPLICANT: McNicol, Patricia J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INPECTIONS USING CATIONIC PEPTIDES ALONE OR
TITLE OF INVENTION: WITH ANTIBIOTICS
ETLE DEPEREMENT. ACCORD.
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PRIOR APPLICATION NUMBER: US/09/462,478A
PRIOR FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: US/60/053,035
PRIOR FILING DATE: 1997-07-18
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 660081.406
CURRENT APPLICATION NUMBER: US/09/030,619B
CURRENT FILLING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                               ITSISLCTPGCKTGALMGCNMKTATCHCSIHVSK 34
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Erfle, Douglas
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Pred. No. 2.
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Pred. No. 1.3e-28;
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.8e-15;
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APPLICANT: KILL,
APPLICANT: Taylor, Robel.
APPLICANT: Erfle, Douglas
APPLICANT: Erser, Janet R.
APPLICANT: West, Michael H.P.
APPLICANT: MCNICOL, PARTYCIA J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INPECTIONS USING CATIONIC PEPTIDES ALONE
TITLE OF INVENTION: WITH ANTIBIOTICS
FILE REFERENCE: 660081.406
CCURRENT APPLICATION NUMBER: US/09/030,619B
CCURRENT APPLICATION NUMBER: US/09/030,619B
CCURRENT FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 232
NUMBER OF SEQ ID NOS: 232
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                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-030-619-208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local Similarity
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APPLICANT: West, Michael H.P.
APPLICANT: McNicol, Patricia J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATIN
TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES
TITLE OF INVENTION: WITH ANTIBIOTICS
FILE REFERENCE: 660081.406C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/290,932
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 96
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CURRENT FILING DATE: 2002-10-18
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TYPE: PRT
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Local Similarity 97.1%;
nes 33; Conservation
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o. US20020035061A1
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97.1%;
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Pred. No. 2.8e-15;
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Pred. No. 2.8e-15;
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PRIOR APPLICATION NUMBER: US/60/053,035
PRIOR APPLICATION NUMBER: US/60/053,035
PRIOR FILING DATE: 1997-07-18
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENETIN Ver. 2.0
SEQ ID NO 9
LENGTH: 56
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Subtilin
US-10-372-098-9
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; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-09-030-619-208
                                                                                                                 US-10-082-618-4
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Publication No. US20030166835A1
GENERAL INFORMATION:
                                                                                                                                                                                  SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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Best Local Similarity
                                      Matches
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Best Local Similarity
                                                                       Query Match
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                                                                                                                                                                                                                   APPLICANT: OLSTEIN, ALAN D.
APPLICANT: FEITTAG, JOELLEN
TITLE OF INVENTION: BACTERIOGIN-METAL COMPLEXES IN THE DETECTION
TITLE OF INVENTION: PATHOGENS AND OTHER BIOLOGICAL ANALYTES
FILE REFERENCE: 7005-0003
CURRENT FILING DATE: 2002-02-22
NUMBER OF SEQ ID NOS: 8
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TITLE OF INVENTION: SUBLANCIN LANTIBIOTIC PRODUCED BY BACILLUS SUBTILIS 168
FILE REFERENCE: 8172-8072
CURRENT APPLICATION NUMBER: US/10/372,098
CURRENT FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: US/09/462,478A
PRIOR FILING DATE: 2000-04-17
PRIOR FILING DATE: 2000-04-17
                                                                                                                         TYPE: PRT ORGANISM: Bacillus subtilis
                                                                                                                                                                     LENGTH: 56
                                                     Local Similarity
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DFNLDLVSVSKKDSGASPRITSTSLCTPGCKTGALMGCNMKTATCHCSI 53
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nilarity 59.2%;
Conservative
                                      Conservative
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                                                   51.6%;
59.2%;
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                                                   Score 157; DB 12;
Pred. No. 1.1e-11;
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Pred. No. 1.1e-11;
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                                    Mismatches
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                                    12;
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                                                                       Length 56;
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US-10-372-098-10
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; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-10-277-233-208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-277-233-208
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                                                                                                                                                                                                                                                              SEQ ID NO 10
LENGTH: 52
TYPE: PRT
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
TITLE OF INVENTION: WITH ANTIBIOTICS
FILE REFERENCE: 660081.406C1
CURRENT APPLICATION NUMBER: US/10/277,233
CURRENT FILING DATE: 2002-10-18
NUMBER OF SEQ ID NOS: 232
SOFTMARE: PastSEQ for Windows Version 3.0
SEQ ID NO 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 51.6%;
Best Local Similarity 59.2%;
Matches 29; Conservative
                                                                                    Matches
                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/372,098
CURRENT FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: US/09/462,478A
PRIOR FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: US/60/053,035
PRIOR FILING DATE: 1997-07-18
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: UNIVERSITY OF MARYLAND
TITLE OF INVENTION: SUBLANCIN LANTIBIOTIC PRODUCED BY BACILLUS SUBTILIS 168
FILE REFERENCE: 8172-8072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Krieger, Timothy J. APPLICANT: Taylor, Robert APPLICANT: Erfle, Douglas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                       ORGANISM: Unknown
                                                                                                           Local
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                                         6 FNLDLVSVSKK---DSGASPRITSTSLCTPGC-KTGA 38
                                                                                    23; Conservative
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Similarity 62.2%;
FNLD-VKVNAKESNDSGAEPRIASKFICTPGCAKTGS 46
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West, Michael H.P.
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Pred. No. 1.1e-11;
8; Mismatches 12;
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                                                                                                         Score 94.5; DB 12; Length 52; Pred. No. 0.00033;
                                                                                  Mismatches
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RESULT 11 US-10-082-618-6

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US-10-082-618-1
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SEQ ID NO 1
LENGTH: 52
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APPLICANT: OLSTEIN, ALAN D.
APPLICANT: FEIRTAG, JOELLE
                                                                                                                                                                                                                                                            Sequence 211, Appropriate Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
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Best Local Similarity
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TITLE OF INVENTION: BACTERIOCIN-METAL COMPLEXES IN THE DETECTION OF
TITLE OF INVENTION: PATHOGENS AND OTHER BIOLOGICAL ANALYTES
FILE REFERENCE: 7005-0003
CURRENT APPLICATION NUMBER: US/10/082,618
CURRENT FILING DATE: 2002-02-22
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/082,618
CURRENT FILING DATE: 2002-02-22
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: FEIRTAG, JOELLEN
TITLE OF INVENTION: BACTERIOCIN-METAL COMPLEXES IN THE DETECTION OF
TITLE OF INVENTION: PATHOGENS AND OTHER BIOLOGICAL ANALYTES
                                                                                                                                                                                                APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: OLSTEIN APPLICANT: FEIRTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 7005-0003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 52
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Staphylococcus gallinarum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 31.1%; Score 94.5; DB 1: Local Similarity 62.2%; Pred. No. 0.00033
                                                                                                                                                                                                                                            INFORMATION:
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                                                                                                                                                          Desnoyers, Luc
Goddard, Audrey
                                                                           Smith, Victoria
                                                                                                                  Godowski, Paul J. Gurney, Austin L.
                                                          Watanabe,Colin K.
                                                                                                                                                                                                                                                                               Application US/10184644
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SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
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Pred. No. 0.00076;
3; Mismatches 6
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RESULT 15
US-10-140-472-67
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; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-184-644-211
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 211
LENGTH: 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 211, Application US/10184634 Publication No. US20030068684A1
                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                       Publication No.
                                                                                                                                                                     Sequence 67,
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APPLICANT:
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APPLICANT:
APPLICANT:
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CURRENT APPLICATION NUMBER: US/10/184,644
CURRENT FILING DATE: 2022-06-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/184,634
CURRENT FILING DATE: 2002-06-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Baker, Kevin P.
                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 708
TYPE: DNA
ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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   PPLICANT
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                                                                                                                    Baker, Kevin P.
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Gerritsen, Mary E. Goddard, Audrey
                                                  Desnoyers, Luc
Filvaroff, Ellen
                                                                                     DeForge, Laura
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                                    Gao, Wei-Qiang
                                                                                                   Beresini, Maureen
                                                                                                                                                                   Application US/10140472
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43.2%;
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Pred. No. 2.3;
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APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Stewart, Timothy A.
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLI
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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: January 12, 2004, 14:22:27; Search time 26 Seconds (without alignments) (without alignments) (without alignments) 210.831 Million cell updates/sec

Title: US-10-082-618-5

Perfect score: 304

Sequence: 1 MSTKDFNLDLVSVSKKDSGA......ALMGCNMKTATCHCSIHVSK 57

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum Match 100%
Listing first 45 summaries

Database: PIR 76:*
1: Dirl:*
2: Dir2:*
3: Pir3:*
4: Dir4:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26					21	20	19							12		_	9	80	-		σı		ω	2	۲	NO.	r
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ACTH/ACTH/ACTF ram probable rnd efflu	unknown protein, 2	DNA topoisomerase	Tid(56) protein -	pyruvate kinase (E	protein T3P18.9 [i	ornithine cyclodea	transcription fact	transcription fact	hypothetical prote	replication licens	conserved hypothet	bud emergence medi	gas1 protein - mou	alcohol dehydrogen

ALIGNMENTS

Alternate name: "Labropoccus Lactus" (Company of the Company of th	RESULT 1

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subtilin precursor - Bacillus subtilis (strain ATCC 6633)
N;Alternate names: SpaS; subtilin A
N;Contains: subtilin B
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                                                                                                                                                                                     RESULT 2
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A;Residues: 24-57 <CHA>
C;Comment: Nisin is secreted
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R;Chan, W.C.; Leyland, M.; Clark, J.; Dodd, H.M.; Lian, L.Y.; Gasson, M.J.; Bycroft, FEBS Lett. 390, 129-132, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Kuipers, O.P.; Rollema, H.S.; de Vos, W.M.; Siezen, R.J.
FEBS Lett. 330, 23-27, 1993
A;Title: Biosynthesis and secretion of a precursor of nisin Z by Lactococcus lactis, A;Reference number: S36142; MUID:93380562; PMID:8370453
A;Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Experimental source: strain 6F3
A;Note: sequence extracted from NCBI backbone (NCBIN:122292, NCBIP:122295)
R;Kuipers, O.P.; Beerthuyzen, M.M.; Siezen, R.J.; de Vos, W.M.
Eur. J. Biochem. 216, 281-291, 1993
Bur. J. Biochem. 216, 281-291, 1993
A;Title: Characterization of the nisin gene cluster nisABTCIPR of Lactococcus lactis. Re
A;Reference number: S36734; MUID:93373937; PMID:7689965
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A; Residues: 1-57 < ENG>
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Superfamily: Su
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ppl. Environ. Microbiol. 58, 3730-3743, 1992

;Title: Biosynthesis of the lantibiotic nisin: genomic organization and membrane

;Reference number: A48951; MUID:93128945; PMID:1482192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lved in nisin biosynthesis.
;Reference number: A40621; MUID:93239683; PMID:8478324
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Am. Chem. Soc. 93, 4634-4635, 1971
Title: The structure of nisin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reference number: A54460; MUID:72072901; PMID:5131162
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;Residues: 1-57 <KUI>
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Best Local
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llarity 98.2%;
Conservative
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Pred. No. 6.9e-27;
0; Mismatches 1
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C;Species: Ba
C;Date: 30-Se
C;Accession:
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A;Contents: annotation
A;Contents: annotation
A;Contents: annotation
A;Contents: annotation
Biochem. J. 23-27, 1993
A;Title: A novel post-translational modification of the peptide A;Reference number: A53265; MUID:93228611; PMID:8471040
A;Reference number: A53265; MUID:93228611; PMID:8471040
A;Contents: annotation; amino-terminal succinylation; ATCC 6633
A;Contents: Annotation; ATCC 6633
F;2-24/Domain: propeptide #status predicted <SIG>
F;25-56/Product: subtilin A #status experimental <MATA>
F;25-56/Product: subtilin B #status experimental <MATB>
F;25-56/Product: subtilin B #status experimental <MATB>
F;25-56/Product: subtilin B #status experimental <MATB>
F;25/Modified site: succinylated amino end (Trp) (in mature form) #link MATB
F;27-31/Cross-link: sn-(2s,6R)-lanthionine (Ser-Cys) #status experimental
F;29/Modified site: dehydroalanine (Ser) #status experimental
F;32-35/Cross-link: (2s,3s,6R)-3-methyl-lanthionine (Thr-Cys) #status experime
F;37-43/Cross-link: (2s,3s,6R)-3-methyl-lanthionine (Thr-Cys) #status experime
F;47-50/Cross-link: (2s,3s,6R)-3-methyl-lanthionine (Thr-Cys) #status experime
F;49-50/Cross-link: (2s,3s,6R)-3-methyl-lanthionine (Thr-Cys) #status experimental
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A;Experimental source: ATCC 6633
R;Chan, W.C.; Bycroft, B.W.; Leyland, M.L.; Lian, L.Y.; Yang, J.C.; Roberts, FEBS Lett. 300, 56-62, 1992
A;Title: Sequence-specific resonance assignment and conformational analysis c A;Reference number: A44571; MUID:92192284; PMID:1547888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Appl. Environ. Microbiol. 60, 2793-2801, 1994
A;Title: Genes involved in self-protection against the lantibiotic subtilin produced by F
A;Reference number: 140511; MUID:94368094; PMID:8085823
A;Accession: 140514
A;Status: preliminary; translated from GB/EMBL/DDBJ
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R;Klein, C.; Kaletta, C.; Schnell, N.; Entian, K.D.
Appl. Environ. Microbiol. 58, 132-142, 1992
A;Title: Analysis of genes involved in biosynthesis of the lantibiotic subtilin.
A;Reference number: A43935; MUID:92171481; PMID:1539969
A;Accession: D43935
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J. Biol. Chem. 263, 9508-9514, 1988
A;Title: Structure and expression of a gene encoding the A;Reference number: A28112; MUID:88243844; pMID:2837490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Kuipers, O.P.; Rollema, H.S.; de Vos, W.M.; Siezen, R.J. FEBS Lett. 330, 23-27, 1993
A;Title: Biosynthesis and secretion of a precursor of nisin A;Reference number: S36142; MUID:93380562; PMID:8370453
A;Contents: annotation
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A;Experimental source: ATCC 6633
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A; Residues: 1-56 <CHU>
A; Residues: 1-56 <CHU>
A; Cross-references: GB: M83944; NID: g143557; PIDN: AAA22772.1;
A; Experimental source: ATCC 6633
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J. Bacteriol. 174, 1417-1422, 1992
A;Title: The subtilin gene of Bacillus subtilis ATCC 66
A;Reference number: A42655; MUID:92138640; PMID:1735728
A;Accession: D42655
                                                                                                                                                                                                                                                                                                                                                                                       C; Superfamily: subtilin precursor c; Keywords: antibiotic; blocked amino end; lanthionine
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A;Residues: 1-56 <KLE2>
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Date: 30-Sep-1989 #sequence revision 12-May-1994 #text change 21-Jul-2000;
Accession: A28112; D42655; D43935; I40514; I39980; S36I42
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基本的語明

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.;Gene: epix
.;Geneme: plasmid
.;Genome: plasmid
.;Superfamily: subtilin precursor
.;Keywords: antibiotic; blocked carboxyl end; lanthionine
.;Keywords: antibiotic; blocked carboxyl end; lanthionine
.;Keywords: antibiotic; blocked carboxyl end; lanthionine
.;Holomain: propeptide #status predicted cPRO>
.;1-30/Domain: propeptide #status experimental cPrimerial + CYS, 1-30-10 + CYS, 1-
gallidermin precursor - Staphylococcus gallinarum C;Species: Staphylococcus gallinarum C;Date: 10-Mar-1994 #Beguence revision 12-May-1994 C;Accession: A61072; A44573; Ā53264 R;Schnell, N.; Entian, K.D.; Goetz, F; Hoerner, T. FEMS Microbiol. Lett. 58, 263-268, 1989 A;Title: Structural gene isolation and prepeptide B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Allgaier, H.; Jung, G.; Werner, R.G.; Schneider, U.; Zaehner, H. Eur. J. Biochem. 160, 9-22, 1986
A;Title: Epidermin: sequencing of a heterodet tetracyclic 21-peptide A;Reference number: A61287; MUID:87030262; PMID:3769923
A;Accession: A61287
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Nature 333, 276-278, 1988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Molecule type: protein
;Residues: 31-52 <ALL>
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;Residues: 1-52 <SCH>
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                                 K.D.; Goetz, F.; Hoerner, T.; Kellner, 58, 263-268, 1989
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Pred. No. 5.5e-11;
8; Mismatches 12
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    prepeptide sequence of gallidermin,
                                                                                                                                                         #text_change 26-Feb-1999
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                                                                              R.; Jung,
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RESULT
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C;Superfamily: subtilin precursor
C;Reywords: antibiotic; blocked carboxyl end; lanthionine
F;1-30/Domain: propeptide #status predicted <PRO>
F;1-30/Domain: propeptide #status experimental <MAT>
F;31-S2/Product: gallidermin #status experimental <MAT>
F;33-37/Cross-link: sn-(25,6R)-lanthionine (Ser-Cys) #status experimental
F;38-41/Cross-link: (25,35,6R)-3-methyl-lanthionine (Thr-Cys) #status experimental
F;44/Modified site: dehydrobutyrine (Thr) #status experimental
F;44-51/Cross-link: sn-(25,6R)-lanthionine (Ser-Cys) #status experimental
F;49-52/Cross-link: (5,Z)-S-(2-aminovinyl)cysteine (Ser-Cys) #status experimental
                                          hypothetical protein XF2284 [imported] - Xylella fastidiosa (strain 9a5c) C;Species: Xylella fastidiosa (strain 9a5c) C;Species: Xylella fastidiosa (strain 9a5c) C;Date: 18 Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000 C;Date: 18 Cylegosion: C82577
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A;Title: Gallidermin: a new lanthionine-containing polypeptide antibiotic.
A;Reference number: A44573; MUID:89030695; PMID:3181159
R; anonymous, The Xyı
Nature 406, 151-157,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: SGD:S0001431
A;Map position: 9L
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A; Residues: 1-995 < LYE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: GB: Z47047;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      госат
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                                                                                                                                                                                                                                                                                                                                                          676 TTDSNGNVYTITTTVPCSSTTATITSCDETGCHVSTSTGÄVVTETVSSKSYTTATVTHCD 735
                                                                                                                                                                                                                                                                                                                                                                                                            w
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            . Similarity
21; Conserv
  The Xylella fastidiosa
151-157, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S50358
                                                                                                                                                                                                                                                         DNGCNTKTVTSECSKETS 753
                                                                                                                                                                                                                                                                                                        --GCNMKTATCHCSIHVS 56
                                                                                                                                                                                                                                                                                                                                                                                                          TKDFNLDLVSVSKKDSGASPRITSTSLCTPGC----KTGALM---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FDLD-VKVNAKESNDSGAEPRIASKFLCTPGCAKTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FNLDLVSVSKK---DSGASPRITSTSLCTPGC-KTGA 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 63; DB
Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 91.5; DB 1
Pred. No. 0.0013;
                            Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            December 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                          of the Organization for Nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2
                                                                                                                                                                                                                                                                                                                                                                                                                                                              25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIPS
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C;Accession: T13954
R;Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bleno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Jungqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigu
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.G.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sal, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; 2
B. Beforence number: Asqaya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein T23F1.6 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t C;Accession: T25169
R;Wilkinson, J.
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                                                                                                                                               MEGF6 protein -
                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Map position: A; Introns: 16/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: clone C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:Z81129; PIDN:CAB03405.1; GSPDB:GN00023; CESP:T23F1.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNAA;Residues: 1-330 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, A;Reference number: Z19990 A;Accession: T25169
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A; Residues: 1-78 <SIM>
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Best Local (
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene: CESP:T23F1.6
                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
nes 12; Conserv
                                                                                                                                                                                                                                                                                               275
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                                                                                                                                                                                                                                                                                            RTTASQQCAPACSTSCNQSCNQPAQMACQPMQNSQCGCQQNYS 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RPDAVSVLTPGCKQAGATLLTLRVRATLYCSTHI 48
                                                                                                                                                                                                                                                                                                                                              RITSTSLCTPGCKTGALMGCN------MKTATCHCSIHVS 56
                                                                                                                                                     rat
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 59.5;
Pred. No. 26;
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Pred. No. 7
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                                                                                                                                                                                                                                                                                                                                                                                                        17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 330;
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DLVSVSKKDSG-ASPR--

----ITSTSLCTPGCKTGALMGCNMKTATCHCS

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A;Cross-references: EMBL:X62528; NID:g57670; PIDN:CAA44388.1; PID:g57671 C;Superfamily: ribonuclease inhibitor; leucine-rich alpha-2-glycoprotein F;280-304/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000 C;Accession: S20597 [C;Accession: S20597]
R;Kawanomoto, M.; Motojima, K.; Sasaki, M.; Hattori, H.; Goto, S.
Biochim. Biophys. Acta 1129, 335-338, 1992
A;Title: cDNA cloning and sequence of rat ribonuclease inhibitor, and tissue A;Reference number: S20597; MUID:92162755; PMID:1536887
A;Accession: S20597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs tagreterence number: Z14126; MUID:98360089; PMID:9693030 A;Accession: T13954 A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                        R;Johnson, D.; Bradshaw, H. submitted to the EMBL Data Library, Februa A;Description: The sequence of C. elegans
                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
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A; Residues: 1-456 < KAW>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-1574 < NAK>
                                                                                       A; Introns:
                                                                                                                                                                                                                                                                                A; Reference number: Z21446
A; Accession: T33970
                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein F46E10.11 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ribonuclease inhibitor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
                                                                                                                               A; Gene: CESP:F46E10.11
                                                                                                                                                                         A: Experimental source:
                                                                                                                                                                                                  A;Cross-references:
                                                                                                                                                                                                                                      A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: T33970
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    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                          Query Match
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                                                                                                                                                                                                                                                          preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   284 LSLAGNELKDEGA--QLLCESLLEPGCQLESLWVKTCSLTAASCPHFCSV
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17; Conserv
    l Similarity
19; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RVTGECLCPPGKTGEDCGADCPEGRWGLGCQEICPACEHGA--SCNPETGTCLC
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                       EMBL:AF125955; PIDN:AAD14711.1; GSPDB:GN00023; ce: strain Bristol N2; clone F46E10
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27.8%;
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                      19.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 39;
8; Mismatches

 Mismatches

  Score 58.5; Di
Pred. No. 19;
4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                   February 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------CKTGALMGCNMKTATCHC 51
                                                                                                                                                                                                                                                                                                                               cosmid F46E10
                                              BB
16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Length 456;
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                                          Length 166;
    Indels 21;
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  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;TILLE: Human homologs of a Drosophila enhancer of split gene
A;Reference number: A56695; MUID:93265135; PMID:1303260
A;Accession: D56695
                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-565 < STO>
                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                              A;Reference number: A84420;
A;Accession: F84721
                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transducin-like enhancer-of-split homolog TLE-3 - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Stifani, S.; B.
Nature Genet. 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Species: Homo sapiens (man)
Date: 21-Jul-1995 #sequence
                                                                                                                                                             Matches
                                                                                                                                                                                                                                         Map
                                                                                                                                                                                                                                                                                                 Cross-references: GB:AE002093; NID:g4582446; PIDN:AAD24830.1; GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Accession: F84721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Superfamily: unassigned WD repeat proteins;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cross-references: GDB:228049; OMIM:600190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene: GDB:TLE3; ESG; ESG3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cross-references: GB:M99438; NID:g307513; PIDN:AAA61194.1; PID:g307514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Molecule type: mRNA
Residues: 1-772 <STI>
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                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Koo, H.; Moffat, K.S.; Crons, D.; Nierman, W.C.; White,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X.; Kaul
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bsition: 2
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LVDPROGTKPELIVCNCTMH 505
                                       LM----GCNMKTATCHCSIH 54
                                                                                SKDFNDFRTKLAGLTSVTKNYFENLVKALENGLADVDSHAACSSKSTSSKSTGCSSKTRE 485
                                                                                                                      TKDFN-----LDLVSVSKK----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; rujii, C.i. (fat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, m, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15pter-15qter
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WD repeat
WD repeat
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28.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       homology <WD2>
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                                                                                                                                                                             Score 58;
Pred. No.
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Pred. No. 71;
                                                                                                                                                         ed. No. 61;
Mismatches
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                                                                                                                                                           20;
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                                                                                                                                                                                              Length 565;
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C;Keywords: phosphoprotein
F;527-560/Domain: WD repeat homology <WD1>
F;613-646/Domain: WD repeat homology <WD3>
F;695-728/Domain: WD repeat homology <WD4>
F;736-769/Domain: WD repeat homology <WD5>
                                                                 В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Miyasaka, H.; Choudhury, B.K.; Hou, E.W.; Li, S.S.L. Eur. J. Biochem. 216, 343-352, 1993
A;Title: Molecular cloning and expression of mouse and human A;Reference number: S35678; MUID:93373944; PMID:8365415
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C;Superfamily: unassigned WD repeat proteins; WD repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-771 < MIY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;108-140/Domain: calmodulin repeat homology <EF1>
F;153-185/Domain: calmodulin repeat homology <EF2>
F;264-251/Domain: protein kinase C zinc-binding repeat homology <KZ1>
F;268-317/Domain: protein kinase C zinc-binding repeat homology <KZ2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:S49760; NID:g261423; PIDN:AAB24434.1; PID:g261424 A;Note: sequence extracted from NCBI backbone (NCBIN:120083, NCBIP:120084) C;Superfamily: human diacylglycerol kinase; calmodulin repeat homology; pro C;Keywords: ATP; calcium binding; duplication; EF hand; phosphotransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Gene cloning, sequence, expression and in situ localization of 80 kDa diacylglyc A;Reference number: A56879; MUID:93095720; PMID:1339302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diacylglycerol kinase (EC 2.7.1.107) alpha - rat
C;Species: Rattus norvegicus (Norway rat)
RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 26-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESG protein
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                                                                 266 SPPENGLDKARGLKKDAPTSPASVASSSSTPSSKTKDL-GHNDKSST
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                                                                                                              STKDFNLDLVSVSKKDSGASPRITSTSLCTPGCKTGALMGCNMKTAT
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Brain Res. 16, 75-87, 1992
                                                                                                                                                           Conservative
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                                                                                                                                                                           Score 57.5;
Pred. No. 92;
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Pred. No. 87;
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                                                                                                                                                                                                Length 771;
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phosphoribosylanthranilate isomerase (EC 5.3.1.24) - Lipomyces starkeyi C;Species: Lipomyces starkeyi C;Date: 06-Dec-1996 #sequence_revision 25-Apr-1997 #text change 20-Jun-

#sequence_revision 25-Apr-1997 #text_change 20-Jun-2000

S70355

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Minimum
Maximum
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Maximum Match 100%
Listing first 45 summaries
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STRAIN=6F3;

MEDLINE=93128945; PubMed=1482192;

Engelke G., Gutowski-Eckel Z., Hammelmann M., Entian K.-D.;

"Blosynthesis of the lantibiotic nisin: genomic organization
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SEQUENCE OF Gross E.;

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Biochem.

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17.9 64 1 17.9 2193 1 17.8 166 1 17.8 8108 1 17.8 808 1 17.8 876 1 17.8 2193 1 17.6 166 1 17.6 3672 1 17.4 298 1 17.4 298 1 17.4 298 1
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ALIGNMENTS
T 1 LACLA LANN LACLA STANDARD; PRT; 57
01-JAN-1990 (Rel. 13, Created) 01-JAN-1990 (Rel. 13, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) Lantibiotic nisin A precursor.
Lactococcus lactis (subsp. lactis) (Streptococcus lactis). Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus. NCBI_TaxID=1360; [1] SEQUENCE FROM N.A.
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EMBL; J04057; AAA88606.1; --
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EMBL; M24527; AAA26948.1; --
EMBL; X68307; CAA48380.1; --
EMBL; W27277; AAA25188.1; --
EMBL; D00696; BAA00501.1; --
EMBL; L16226; AAA25189.1; --
EMBL; M79445; AAA25198.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tabeling of bacteriocins: NMR resonance assignments of leucocin A from Leuconostoc gelidum and nisin A from Lactococcus lactis."; Biochemistry 32:310-318(1993).

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                    EMBL;
PIR;
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Hilbers C.W., van de Ven F.J.;
"NMR and circular dichroism studies
                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aqueous environments." FEBS Lett. 319:189-194
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van de Ven F.J., van den Hooven H.W., Koning
"NMR studies of lantibiotics. The structure
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MEDLINE=72072901; PubMed=5131162;
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MISCELLANEOUS: USED AS A FOOD PRESERVATIVE.

MISCELLANEOUS: THE NISA GENE IS FOUND BOTH ON CHROMOSOMAL AND PLASMID DNA. THE SEQUENCES REPORTED ARE ABSOLUTELY IDENTICAL PLASMID DNA. THE SEQUENCES REPORTED ARE ABSOLUTELY IDENTICALS.

SIMILARITY: STRUCTURAL SIMILARITY TO OTHER TYPE A LANTIBIOTICS.
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n. Chem. Soc. 93:4634-4635(1971).
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an email to license@isb-sib.ch).
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J. 283:413-420(1992).
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G.L., Henkel T.,
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W., Fogolari F.,
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in aqueou
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Best Local S
Matches 56
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SEQÜENCE
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SEQUENCE FROM N.A.
STRAIN-NIZO 22186;
MEDLINE-92037612; PubMed=1935953;
MEDLINE-92037612; PubMed=1935953;
                                                                                                                                   MEDLINE=95352820; PubMed=7626780; Timmonen T., Ye S., Ra R., Olao M., Paulin L., Saris P.E.J. "The codon usage of the nisz operon in Lactococcus lactis a non-lactococcal origin of the conjugative nisin-sucrose
                                                                                                                                                                                                                       form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LANZ LACLA P29559;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LACLA
                                                                                                                          transposon.";
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"Genetic evidence th
                                                                                                                                                                                                                                                     STRAIN=JCM 7638;
                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                           Lactococcus lactis (subsp. Bacteria; Firmicutes; Lacto
                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1993
15-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1993
                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                natural nisin variant.
                                                                                                                                                                                                                                                                                                         "Identification and characterization
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                                                                                                                                                                                                                                                                                                                                                                                                                          Lantibiotic
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                                                                                                                                                                                                                                                                                                                   VOS W.M.;
                                                                Seq. 5:203-218(1995).

FUNCTION: LANTHIONINE-CONTAINING PEPTIDE ANTIBIOTIC (LANTIBIOTIC)

ACTIVE ON GRAM-POSITIVE BACTERIA. THE BACTERICIDAL ACTIVITY OF

LANTIBIOTICS IS BASED ON DEPOLARIZATION OF ENERGIZED BACTERIAL

CYTOPLASMIC MEMBRANES, INITIATED BY THE FORMATION OF AQUEOUS
        and cleavage of the mod
SIMILARITY: STRUCTURAL
                  PTM: Maturation of lantibiotics involv
Thr, and Ser into dehydrated AA and th
bonds with cysteine. This is followed
and cleavage of the modified precursor
                                                              TRANSMEMBRANE PORES.
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                                                                                                                                                                                                                                                                                                                                                                                 TaxID=1360;
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(Rel.
(Rel.
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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        SIMILARITY TO O
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Pred. No. 8.2e-31;
); Mismatches 1
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DHB (2,3-DIDEHYDROBUTYRINE).
DHA (2,3-DIDEHYDROALANINE).
DHA (2,3-DIDEHYDROALANINE).
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Beta-methyllanthionine
Beta-methyllanthionine
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                               membrane
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                              enzymic conversion
ation of thioether
brane translocation
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(Thr-Cys).
(Thr-Cys).
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MEDLINE=92171481; PubMed=1539969; Klein C., Kaletta C., Schnell N., "Analysis of genes involved in bio subtilin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BACSU
                                                                                                                                                                 STRAIN=ATCC 6633 / LETT / MEDILINE=92138640; PubMed=1735728; Chung Y.J., Steen M.T., Hansen J.N.; The subtilin gene of Bacillus subtilis ATCC 6633 is encoded "The subtilin gene of Bacillus abbtilis ATCC 6633 is encoded the subtiline a homolog of the hemolysin B transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contentites requires a license agreement (See http://www.isb-sib.ch/ar or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=ATCC 6633 / LH45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus subtilis.
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1989 (Rel. 11,
15-SEP-2003 (Rel. 42,
Lantibiotic subtilin
                                                                                                                                                                                                                                                                                                                                                    subtilin,
                                                                                                                                                                                                                                                                                                                                                                                           Banerjee
                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=88243844; PubMed=2837490;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P10946;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=1423;
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the European Bioinformatics Institute
                                                                                                                                                     Bacteriol.
                                                                                                                                                                                                                                                                                                                                   Biol.
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                                                                                                           FROM
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                                                                                                                                                                                                                                                                                                                                   Chem.
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                                                                                                                                                                                                                                                                                                                                                                                           Hansen J.N.;
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662586618600
                                                                                                             N.A.
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                                                                                                                                                   174:1417-1422(1992)
                                                                                                                                                                                                                                                                                                                               expression of a gene enc
all protein antibiotic.";
263:9508-9514(1988).
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96.5%;
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Pred. No. 6.2e
1; Mismatches
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Beta-methyllanthionine (Thr-Cys).
DHB (2,3-DIDEHYDROBUTYRIB).
DHA (2,3-DIDEHYDROALANINE).
DHA (2,3-DIDEHYDROALANINE).
DHA (2,3-DIDEHYDROALANINE).
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Beta-methyllanthionine
Beta-methyllanthionine
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                             Entian K.-D.;
osynthesis of the
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on update)
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                                 lantibiotic
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EMBL; J03767; AAA22840.1; -.
EMBL; M86869; AAA22840.1; -.
EMBL; M83944; AAA22772.1; -.
EMBL; M939263; AAA22778.1; -.
EMBL; U09819; AAB91589.1; -.
PIR; A28112; NIBSSA.
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Antibiotic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=89276381; PubMed=2471644; Schueller F., Benz R., Sahl H.-G.; "The peptide antibiotic subtilin act voltage-dependent multi-state pores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gross E., Kiltz H.H., Nebelin E.; "Subtilin, VI: the structure of subtilin."; "Subtilin, VI: the structure of subtilin."; "Foppe-Seyler's Z. Physiol. Chem. 354:810-81
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Gross E., Kiltz H.H.,
"Subtilin, VI: the st:
                                                                                                                                                Pfam; PF02052; Gallidermin; PRINTS; PR00324; NISIN.
                                                                                                                                                                                                                                                                                                                                                                                     between
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MEDLINE=93167833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Sequence-specific resonance assignment and conformational analysis of subtilin by 2D NMR."; FEBS Lett. 300:56-62(1992).
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                                                                                                                                                                             InterPro; IPR006079;
InterPro; IPR000446;
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                                                                                                                                                                                                                                                                                                                                                      s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                            Thr, and Ser into dehydrated AA and the formation of thi bonds with cysteine. This is followed by membrane transl and cleavage of the modified precursor.
MISCELLANEOUS: SUBTILIN ACTIVITY IS OBSERVED DURING STAIPHASE, BUT NOT DURING EXPONENTIAL GROWTH.
SIMILARITY: STRUCTURAL SIMILARITY TO OTHER LANTIBIOTICS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTM: Maturation of lantibiotics involves the enzymic conversion Thr, and Ser into dehydrated AA and the formation of thioether bonds with cysteine. This is followed by membrane translocation
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FUNCTION: LANTHIONINE-CONTAINING PEPTIDE ANTIBIOTIC (LANTIBIOTIC)
ACTIVE ON GRAM-POSITIVE BACTERIA. THE BACTERICIDAL ACTIVITY OF
LANTIBIOTICS IS BASED ON DEPOLARIZATION OF ENERGIZED BACTERIAL
CYTOPLASMIC MEMBRANES, INITIATED BY THE FORMATION OF AQUEOUS
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Bycroft B.W., Leylands M.L.,
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.H., Nebelin E.;
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      4255433564
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                                                     EMBL; X07840; CAA30689.1; -.
EMBL; X07840; CAA30690.1; -.
EMBL; X62386; CAA4252.1; -.
EMBL; X62386; CAA01070.1; -.
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STRAIN=TU 3298 / DSM 3095;
MEDLINE=92155237; PubMed=1740156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Prepeptide sequence of epidermin, a ribosomally antibiotic with four sulphide-rings."; Nature 333:276-278(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schnell N., Entian K.-D., Schneider U., Kellner R., Jung G.;
                                                                                                                       or send an
                                                                                                                                             the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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Bacteria; F:
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"Analysis of genes involved in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                nterPro;
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SIMILARITY: STRUCTURAL SIMILARITY TO OTHER TYPE A LANTIBIOTICS.
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                                                                                                                                                         the Swiss Institute of Bioinformatics and the EMBL outstat
pean Bioinformatics Institute. There are no restrictions on
non-profit institutions as long as its content is in no
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IPR006078; Gallidermin.
IPR006079; Lan_dom.
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                                                                                                                       email to license@isb-sib.ch).
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SEQUENCE
                   PIR; A61072; EPSGD.
InterPro; IPR006078; Gallidermin.
InterPro; IPR006079; Lan dom.
InterPro; Gallidermin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus gallinarum.
Staphylococcus gallinarum.
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                                                                                                                                                                                                                                                        STRUCTURE BY NMR. MEDLINE=92032577;
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           PRINTS; PR00323; GALLIDERMIN.
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                                                                                                                                                                                                                                                                                                                                                         STRAIN=TU
                                                                                                                                                                                                                                                                                                                                                                                        Schnell N., Entian K.-D., Goetz F., Hoerner T., Kellner R., Jung G "Structural gene isolation and prepeptide sequence of gallidermin, new lanthionine containing antibiotic.";
FEMS Microbiol. Lett. 49:263-267(1989).
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                                                                                                                                                                                                                   'The solution structure of the lantibiotic gallidermin.";
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                                                                                                                                                                                                                                                                                           "Gallidermin: a new lanthionine-containing Eur. J. Biochem. 177:53-59(1988).
                                                                                                                                                                                                                                                                                                                                                                    EQUENCE
                                                                     cleavage of the modified precursor. SIMILARITY: STRUCTURAL SIMILARITY 1
                                                                                                                                                      FUNCTION: LANTHIONINE-CONTAINING REPTIDE ANTHBIOTIC (LANTHBIOTIC) ACTIVE ON GRAM-POSITIVE BACTERIA. THE BACTERICIDAL ACTIVITY OF LANTIBIOTICS IS BASED ON DEPOLARIZATION OF EMERGIZED BACTERIAL CYTOPLASMIC MEMBRANES, INITIATED BY THE FORMATION OF AQUEOUS
                                                                                            Thr, and Ser into dehydrated AA and the formation of thioether bonds with cysteine. The C-terminal lanthionine undergoes decarboxylation. This is followed by membrane translocation and
                                                                                                                               TRANSMEMBRANE PORES.

PTM: Maturation of lantibiotics involves the enzymic
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Pred. No. 2.
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DHB (2,3-DIDEHYDROBUTYRINE).
8B1AD2875BF16D6D CRC64;
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Beta-methyllanthionine
Lanthionine (Ser-Cys).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                            Folkers G.,
                                                                                                                                                                                                                                                                                                                               Zaehner H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
                                                                      TO OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ₿
                                                                                                                                                                                                                                                                                                       polypeptide
                                                                                                                                                                                                                                            Gibbons W.A.,
                                                                                                                                                                                                                                                                                                                               Schnell N.,
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                                                                      TYPE
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                                                                     A LANTIBIOTICS
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                                                                                                                     nic conversion of thioether
                                                                                                                                                                                                                                                                                                        antibiotic.";
                                                                                                                                                                                                                                                                                                                               Entian K.-D.,
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Best Local S
Matches 17
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Best Local
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CROSSLNK
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                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                 Karaya K., Taketo A.; "Gene cluster of lantibiotics producing by Streptococcus pyogenes."; Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOD_RES
                                                                                     CHAIN
                                                                                                                 EMBL; AB030831; BAB08162.1; -. EMBL; AE006552; AAK33966.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRPY
                                                                                                                                                                the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pyogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9FDV1;
16-OCT-2001
                                                                           SEQUENCE
                                                                                                PROPEP
                                                                                                        Antibiotic;
                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1314;
                                                                                                                                                                                                                                                                                                                                                                                                                            SRTA OR SPY1083.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Lantibiotic srtA precursor.
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16-OCT-2001
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                                     l Similarity 56.
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                KDFNLDLVSVSKKDSGASPRITSTSLCTPG 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FNLDLVSVSKK---DSGASPRITSTSLCTPGC-KTGA
KDFDLDL-KTNKKDT-ATPYVGSRYLCTPG
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(Rel. 40,
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ilarity 62.2%;
Conservative
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31
33
38
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49
44
AA;
                                                                                                      Bacteriocin; Lantibiotic;
                                                                           AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                          5219 MW;
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52
52
                                              23.7%;
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Last annotation update)
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                                      5
                                    Score 72; DB
Pred. No. 0.01
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 5.26
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lanthionine (Ser-Cys).
S-(2-aminovinyl)-D-cysteine (Ser-Cys).
DHB (2,3-DIDEHYDROBUTYRINE).
                                                                           3775CC54B8A2B00F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 91.5;
Pred. No. 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8584C0040AB4786D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Beta-methyllanthionine (Thr-Cys).
                                                                                     LANTIBIOTIC SRTA
                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lanthionine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LANTIBIOTIC GALLIDERMIN.
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                                                                                                       Complete
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                                              DB 1;
0.013;
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                                                                            CRC64;
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                                                        Length 46;
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RESULT 7

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RESULT 8
E4L5 HH
AC Q9HCM4
DT 16-OCT
DT 15-SEP
DE Band 4
GN EPB41L
OS Homo 8
OC Eukary
OC Mammal
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Best Local :
                                          Q9HCM4; Q9H975;
16-OCT-2001 (Rel. 40, C
16-OCT-2001 (Rel. 40, L
15-SEP-2003 (Rel. 42, L
Band 4.1-like protein 5
EPB41L5 OR KIAA1548.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P40442;
01-FEB-1995
01-FEB-1995
15-SEP-2003
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CARBOHYD
CARBOHYD
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SGD; S0001431; YIL169C.
THERPERO; IPRO04088; Chmtaxis_TRANSDUC_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institute. There are no restrictions modified and this statement is not removed. Usage by and for commentities requires a license agreement (See http://www.inh.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Churcher C.M., Bowman S., Badcock K., Bankier A., Brown D., Chillingworth T., Connor R., Devlin K., Gentles S., Hamlin N., Harris D.E., Horsnell T., Hunt S., Jagels K., Jones M., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Rowley Skelton J., Smith V., Walsh S., Whitehead S., Barrell B.G.; "The nucleotide sequence of Saccharomyces cerevisiae chromosome Nature 387.84-87(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
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01-FBB-1995 (Rel. 31, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Hypothetical 99.7 kDa protein in SDL1 5'region
YIL169C OR YI9402.07C.
  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YIQ9
                               Homo sapiens (Human)
                                                                                                                               E4L5 HUMAN
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z46921; CAA87023.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-S288c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Contains 1 methyl-accepting transducer domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ypothetical protein; IGNAL 1 2
                                                                                                                                                                                                                                                             676
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                                                                                                                                                                                                                                                                                  TKDFNLDLVSVSKKDSGASPRITSTSLCTPGC----KTGALM---
                                                                                                                                                                                                     DNGCNTKTVTSECSKETS
                                                                                                                                                                                                                                                             TTDSNGNVYTITTTVPCSSTTATITSCDETGCHVSTSTGAVVTETVSSKSYTTATVTHCD 735
                                                                                                                                                                                                                                                                                                                                                                           995 AA;
                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / AB972;
                                                                                                                               STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                     995
253
26
35
  ; Chordata;
; Primates;
                                                                                                                                                                                                                                                                                                                                 20.7%;
                                                                                                                                                                                                                                                                                                                                                                           99735 MW;
                                                                                                   Created)
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HYPOTHSTICAL PROTEIN YIL169C.

METHYL-ACCEPTING TRANSDUCER.

N-LINKED (GLCNAC. ...) (POTENTI

N-LINKED (GLCNAC. ...) (POTENTI
                                                                                       sequence
                                                                                                                                                                                                                               56
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                                                                                                                                                                                                                                                                                                                                Score 63; DB 1; Length 995; Pred. No. 4.6;
  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
(POTENTIAL)
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RESULT
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P29315;
                                                                                                                                               Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; MCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00660; FERM_1; 1.
PROSITE; PS00661; FERM_2; 1.
PROSITE; PS50057; FERM_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between the Swiss Institute of Bioinformat:
the European Bioinformatics Institute. These
use by non-profit institutions as long a
modified and this statement is not removed.
entities requires a license agreement (See)
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01-DEC-1992 (Rel. 24, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000299; Band ...
Pfam; PF00373; Band 41; 1.
PRINTS; PR00935; BAND41.
SMART; SM00295; B41; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AK023019; BAB14360.1; -. EMBL; AB046768; BAB13374.1; -.
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                                                                                                   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      XVIII. The complete sequences of 100 ne code for large proteins in vitro."; DNA Res. 7:273-281 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20450683; PubMed=10997877;
Nagase T., Kikuno R., Nakayama M., Hirosawa M., Ohara O.;
"Prediction of the coding sequences of unidentified human genes.
XVIII. The complete sequences of 100 new cDNA clones from brain which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IBOGAI T., Ota T., Hayashi K., Sugiyama T.,
Nishikawa T., Nagai K., Sugano S., Aotsuka S.
Matsunawa H., Ishii S., Kawai Y., Saito K.,
Nakamura Y., Nagahari K., Masuho Y., Sasaki
                                                    MEDLINE=92162755; PubMed=1536887;
                                                                                                                                                                                                                                Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                    Ribonuclease
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                          Kawanomoto M., Motojima K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       732 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43
669
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                                                                                                                                                                                                                                                                                    inhibitor
     and
                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
tojima K., Sasaki M., Hattori H., Goto S sequence of rat ribonuclease inhibitor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81758 MW;
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29.4%;
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Pred. No. 5.9;
12; Mismatches
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GGAMSIAGCEMLLTGKEGHGNKDGISLISPPAPFLYDAV
TSSGPILAEEAVLKQKCLLTTEL -> LWSHFGRRSCPEAE
VFTDH (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76D5BD8CE099E761 CRC64;
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Saito K., Yamamoto J., Wakamatsu A.,
., Sasaki N.;
                                                                                                                                                                                                                                                                                                                                   update)
                                                                                                                                                                                                                                                                                                                                                                                                            456
                                                                                                                                                                                                                                                                                                         update:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    There are no restrictions on ong as its content is in no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
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and tissue
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P55947;
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                          MEDLINE=97373947; PubMed=9230430;
Dallinger R., Berger B., Hunziker P.E., Kaegi J
"Metallothionein in snail Cd and Cu metabolism.
Nature 388:237-238(1997).
                                                                                                                                                                                                                                                                                                                                                                         01.NOV-1997 (Rel. 35, Created)
01.NOV-1997 (Rel. 35, Last seg
28.FEB-2003 (Rel. 41, Last ann
Copper-metallothionein (Cu-MT)
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InterPro; IPR007091; LRR RNinh.
InterPro; IPR003590; LRR_RNinh_sub.
Pfam; PF00560; LRR; 4.
SMART; SM00368; LRR_RI; 1.
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                                                                                                                                                         SEQUENCE.
TISSUE=Mantle;
                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Mollusca; Gastropoda;
Sigmurethra; Helicoidea; Helicidae; Helix
                                                                                                                                                                                                                                                                                                                                                  Helix pomatia (Roman snail) (Edible snail).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HELPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X62528; CAA44388.1; -. PIR; S20597; S20597. HSSP; P10775; 2BNH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <del>-</del> <del>-</del> <del>-</del> <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochim.
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FUNCTION: INHIBITOR OF PANCREATIC RNASE AND ANGIOGENIN. MAY ALSO FUNCTION IN THE MODULATION OF CELLULAR ACTIVITIES.
SUBGUNIT: FORMS A TIGHT ONE-TO-ONE COMPLEX WITH THE RNASE.
SUBCELLULAR LOCATION: Cycoplasmic.
SUBCELLULAR LOCATION: Cycoplasmic.
TISSUE SPECIFICITY: BRAIN, HBART, LUNG, LIVER, SPLEEN, TESTES ANI
KIDNEY, HIGHEST IN THE LUNG AND LOWEST IN THE HEART.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: Contains 15 leucine-rich (LRR) repeats.
                                                                                                                                                                                                                                                       TaxID=6536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a centre the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               284 LSLAGNELKDEGA--QLLCESLLEPGCQLESLWVKTCSLTAASCPHFCSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
   METALLOTHIONEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49905 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
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8518E5B1F09E5998 CRC64;
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ARE INVOLVED IN THE CELLULAR
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                                                                                           Kaegi J.H.R.;
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                                                                                                                                                                                                                                                                                                                  Pulmonata; Stylommatophora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Length 456;
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Best Local S
Matches 12
                MEDLINE=20456683; PubMed=10997877;
Nagase T., Kikuno R., Nakayama M., Hirosawa M., Ohara O.;
"prediction of the coding sequences of unidentified human
XVIII. The complete sequences of 100 new cDNA clones from
code for large proteins in vitro.";
DNA Res. 7:273-281(2000).
                                                                                                                                                                                                                                                       TLE3_HUMAN STANDARD; PRT; 772 AA. Q04726; QBIVV6; QBWVR2; Q9HCM5; Q1-FEB-1994 (Rel. 28, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) 17-ransducin-like enhancer protein 3 (ESG3).
                                                                                                                                                                                                                                                                                                                         HUMAN
                                                                                                                                                              TISSUE=Fetal brain;
MEDLINE=93265135; P
                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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                                                                                                                      Artavanis-Tsakonas S.;
"Human homologs of a Drosophila enhancer of split gene product define
a novel family of nuclear proteins.";
                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                  TLE3 OR KIAA1547.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                 TISSUE=Brain;
                                                                                          SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                       Stitani
                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUESTRATION OF TOXIC METAL IONS AND REGULATION OF ESSENTIAL TRACE ELEMENTS. THIS ISOFORM BINDS EXCLUSIVELY COPPER. DOMAIN: 14 (CYSTEINE RESIDUES ARE ARRANGED IN C-X-C GROUPS. THESE ARE THOUGHT TO BE THE METAL-BINDING SITES IN OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                METALLOTHIONEINS
                                                                                                                                                                                                                                                                                                                                                                  18
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                                                                                                                                                                                                                                                                                                                                                                                                         1 Similarity
12; Conser
                                                                                                                                                     S., Blaumueller C.M., Redhead N.J., Hill R.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PR00438; GFCYSKNOT
                                                                                                                                                                                                                                                                                                                                                                                 CTPGCKTGALMGCNM-KTATCHCS
                                                                                                                                                                                                                                                                                                                                                                 CGNDCKCGA--GCNCDRCSSCHCS 39
                                                                                                             ily of nuclear proteins.";
2:119-127(1992).
                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=1303260;
                                                                                                                                                                                   (ISOFORM 1).
(ISOFORMS 3 AND 4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                6205 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                        Score 58.5; DB 1;
Pred. No. 0.87;
3; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COPPER.
96CC1998B7E12297 CRC64;
                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                      genes.
brain which
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RA Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA HOpking R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., RA Hopking R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., RA Schapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RICHARD S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., RA Richards S., Worley M.M., Sodergren B.J., Lu X., Gibbs R.A., RA Richards J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A., RA Fahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A., RA Hillon D.K., Maran M., Green E.D., Dickson M.C., RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Cheer B.D., Dickson M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Transducin-like enhancer of split proteins, the human homologs of Drosophila groucho, interact with hepatic nuclear factor 3beta.";
J. Biol. Chem. 275:18418-18423(2000).

-:- FUNCTION: Transcriptional corepressor that binds to a number of transcription factors. Inhibits the transcriptional activation mediated by CTNNB1 and TCF family members in Wnt signaling. The effects of full-length TLE family members may be modulated by association with dominant-negative AES (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Granner D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 324-338 AND 521-531, MEDLINE=20309797; PubMed=1074819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Pancreas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22388257;
                                                                                                                                                                                                                                                                                                                                                                  IsoId=904726-4; Sequence=VSP_007023, VSP_007024, VSP_006790; TISSUE SPECIFICITY: Placenta and lung. SIMILARITY: Contains 7 MD repeats. SIMILARITY: BELONGS TO THE GROUCHO/TLE FAMILY OF WD-REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: Homooligomer and heterooligomer with other family members. Binds LEF1, TCF7, TCF7L1 and TCF7L2 (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Event=Alternative splicing; Named isoforms=4; Comment=Experimental confirmation may be lacking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Binds FOXA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         isoforms;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=Q04726-3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=Q04726-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=Q04726-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09797; PubMed=10748198;
Waltner-Law M., Yamada K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: Nuclear.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence=VSP_006789, VSP_006790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence=VSP_006788;
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                                                                                                                                                                                                                                                                                           a collaboration -
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PIR; D56695; D56695. Genew; HGNC:11839; T EMBL; BC015729; -; NOT_ANNO' EMBL; BC041831; AAH41831.1; EMBL; M99438; AAA61194.1; EMBL; AB046767; BAB13373. muse by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See lor send an email to license@isb-sib.ch). This SWISS-PROT entry is copyright. It is produced through between the Swiss institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content GO:0005634; GO:0007397; 600190; C:nucleus; TAS. P:histogenesis 73.1; ALT INIT. ANNOTATED CDS. and organogenesis; TAS (See http://www.isb-sib Usage by and for commercia no

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-KDGA_RAT STANDARD; PRT; 727 AA.

PS1556;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
11-OCT-2001 (Rel. 40, Last annotation update)
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Pfam; PF03920; WD40; 6.

ProDom; PD000018; WD40; 1.

SMART; SM00320; WD40; 7.

SMART; SM00320; WD REPEATS 1; 2.

PROSITE; PS50082; WD REPEATS 7; 2.

PROSITE; PS50082; WD REPEATS REGION; 2.

PROSITE; PS50294; WD REPEATS REGION; 2.

Transcription regulation; Repressor; Nuclear protein; Repeat; Phosphorylation; Wnt signaling pathway;
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NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
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WD 5.
WD 5.
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ProDom; PD005043; DAGKC; 1.
ProDom; PD0050112; EF-hand; 1.
SMART; SM00109; C1; 2.
SMART; SM00045; DAGKa; 1.
SMART; SM00046; DAGKC; 1.
SMART; SM00054; EFh; 2.
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CA_BIND
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DOMAIN
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or send an email +
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Goto K., Watanabe M., Kondo H., Yuasa H., Sakane F., Kanoh H.;
"Gene cloning, sequence, expression and in situ localization of 80 kDa diacylglycerol kinase specific to oligodendrocyte of rat brain.";
Brain Res. Mol. Brain Res. 16.75-87(1992).
-!- FUNCTION: UPON CELL STIMULATION CONVERTS THE SECOND MESSENGER DIACYLGLYCEROL INTO PHOSPHATIDATE, INITIATING THE RESYNTHESIS
                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                            Pfam; PF00036; efhand;
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InterPro; IPR001756; DAGKG.
InterPro; IPR001206; DAGKG.
InterPro; IPR002048; EF-hand.
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                                                                                                                                                                                   Transferase; Kinase;
                                                                                                                                                                                                                                                                                                                                          Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tities requires a license agreement (S send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHOSPHORYLATED BY PROTEIN KINASE SUBUNIT: Monomer (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diacylglycerol 3-phosphate. ENZYME REGULATION: STIMULATED BY
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                           16;
                                                                                                                                                         Multigene
121
                                       Similarity
                                                                                                                                                                              PS00479; DAG PE BIND DOM 1; 2
PS50081; DAG PE BIND DOM 2; 2
PS500818; EF HAND; 2.
PS00018; EF HAND; 2.
MSTKDFNLDLVSVSKKDSGASPRITSTSLCTPGCKTGALMGCNMKTAT--
                                                                         512
727
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                           Conservative
                                                                             AΑ;
                                                                                                                                                                     family.
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177
251
317
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693
                                                                             82198
                                     18.9%;
                                                                             MW;
                                                                                      EF-HAND 1 (PROBABLE).
EF-HAND 2 (PROBABLE).
PHORBOL-ESTER AND DAG BI
PHORBOL-ESTER AND DAG BI
CATALYTIC-A (POTENTIAL).
CATALYTIC-B (POTENTIAL).
                        Score 57.5; I
Pred. No. 16;
6; Mismatches
                         6
                                                                             B5A248ADD2F61C1D CRC64;
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C (BY SI
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SIMILARITY).
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J. Neurochem. 74:1838-1847(2000).

-!- FUNCTION: Transcriptional corepressor that binds to a number of the endough of the property of the property of the transcriptional activation. The
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DOMAIN
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Pfam; PF00400; WD40; 6.
ProDom; PD000018; WD40; 1.
SWART; SW00320; WD40; 7.
PROSITE; PS0002; WD REPEATS 2; 2.
PROSITE; PS50082; WD REPEATS 2; 2.
PROSITE; PS50294; WD REPEATS REGION; 2.
                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
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                                                                                                                                                                                                                                                                                                                                                                       the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                         DOMAIN
                                                                                                                                   WD repeat;
                                                                                                                                                                                                                                                                                                                                                                                   between the
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15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Transducin-like enhancer protein 3 (TTLE3).
                                                                                                                                                   Transcription
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                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity).
SUBCELLULAR LOCATION: Nuclear.
SUBCELLULAR LOCATION: Nuclear.
TISSUE SPECIFICITY: Highly expressed in adrenal gland, intestine, kidney, lung, ovary and thyroid. Detected at levels in pituitary, hippocampus, cortex, cerebellum an INDUCTION: By kainic acid in the dentate gyrus.
SIMILARITY: Contains 7 WD repeats.
SIMILARITY: BELONGS TO THE GROUCHO/TLE FAMILY OF WD-REF
                                                                                                                                                                                                                                                                                                                                                                s SWISS-PROT entry is copyright. It is produced through a collab
ween the Swiss Institute of Bioinformatics and the EMBL outst
burgean Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mediated by CTNNB1 and TCF family members in Wnt signaling. The effects of full-length TLE family members may be modulated by association with dominant-negative AES (By similarity). SUBUNIT: Homooligomer and heterooligomer with other family members. Binds LEF1, TCF7, TCF7L1, TCF7L2 and FOXA2 (By
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                                                                   LOCALIZATION SIGNAL (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOD_RES
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STRAIN-CD-1;
MEDLINE=93373944; PubMed=8365415;
MEDLINE=9337394;
MEDLINE=9337494;
MEDLINE=9337
"Analysis of the mouse transcriptome 60,770 full-length cDNAs."; Nature 420:563-573(2002).
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Mammalia; Eutheria;
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STRAIN=C57BL/6J; TISSUE=Testis;
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A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Vallalon D.K., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Holterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Chang C.M., Schmutz J., Myers R.M.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Rés. 29:1410-1419(2001).

-!- FUNCTION: Transcriptional corepressor that binds to a number of transcription factors. Inhibit the transcriptional activation mediated by CTWNB1 and TCF family members in Wnt signaling. The effects of full-length TLE family members may be modulated by association with dominant-negative AES (By similarity). May planscript that the signal sign
                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                             EMBL; X73360; CAA51770.1; -. EMBL; AK031322; BAC27347.1; -. EMBL; BC006672; AAH06672.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -
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MEDLINE=22388257;
                                                                                           InterPro; IPR005617; TLE N.
InterPro; IPR001680; WD40.
Pfam; PF03920; TLE N; 1.
Pfam; PF00400; WD40; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brantjes H., Roose J., van De Wetering "All Tcf HMG box transcription factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERACTIONS WITH LEF1; TCF7; TCF7L1 AND MEDLINE=21169341; PubMed=11266540;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 323-771 FROM N.A. (ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note=No experimental confirmation available;
TISSUE SPECIFICITY: Expressed only in testis.
SIMILARITY: Contains 7 WD repeats.
SIMILARITY: BELONGS TO THE GROUCHO/TLE FAMILY OF WD-REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Nuclear.
ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Na
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  an important role during spermatogenesis.
SUBUNIT: Homooligomer and heterooligomer with other family
members. Binds FOXA2 (By similarity). Binds LEF1, TCF7, TC
                                                                                                                                                                                                                       S35681; S35681.
MGI:104634; Tle3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=Q08122-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=Q08122-2; Sequence=VSP_007025;
                                  PD000018;
; PS00678;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the Swiss Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tumor;
WD40; 1.
WD_REPEATS_1;
WD_REPEATS_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          right. It is produced through of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                        (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M., Clevers H. interact with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              There are no restrictions ng as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCF7L2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Usage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        commercia]
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RESULT 15
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                  ENTK MOUSE
P97435;
                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created, 01-NOV-1997 (Rel. 35, Last sequence up 28-FEB-2003 (Rel. 41, Last annotation comparidase (EC 3.4.21.9) (Enterol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
SEQUENCE
                                                                                                               small intestine during development.";

Am. J. Physiol. 274:G342-G349(1998)
-I- FUNCTION: RESPONSIBLE FOR INITIATING ACTIVATION OF PANCREATIC PROTECLYTIC PROENZYMES (TRYPSIN, CHYMOTRYPSIN AND CARBOXYPEPTIDASE A). IT CATALYZES THE CONVERSION OF TRYPSINOGEN TO TRYPSIN WHICH IN TURN ACTIVATES OTHER PROENZYMES INCLUDING CHYMOTRYPSINOGEN, PROCARBOXYPEPTIDASES, AND PROELASTASES (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOD_RES
            ++
                                                                                                                                                                                       MEDLINE=98147142; PubMed=9486188;
Yuan X., Zheng X., Lu D., Rubin D.C., Pung C.Y.M., Sadle
"Structure of murine enterokinase (enteropeptidase) and
                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                Enteropeptidase (EC PRSS7 OR ENTK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Repeat; WD :
                                                                                                                                                                                                                         STRAIN=C57BL/6; TISSUE=Duodenum,
                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spermatogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPEAT
SUBCELLULAR LOCATION: Type II membrane protein (Proleym. THE CHAINS ARE DERIVED FROM A SINGLE PRECURSOR CLEAVED BY A TRYPSIN-LIKE PROTEASE (BY SIMILARITY). SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
SIMILARITY: Contains 2 LDL-receptor class A domains.
SIMILARITY: Contains 2 CUB domains.
                                                                                    trypsinogen.
SUBUNIT: HET
                                                               SIMILARITY).
                                                                          MULTIDOMAIN (HEAVY)
                                                                                                        CATALYTIC ACTIVITY: Selective cleavage
                                                                                                                                                                                                                                                                                                                                                                                                                 266 SPPENGLDKARGLKKDAPTSPASVASSSSTPSSKTKDL-GHNDKSST
                                                                                                                                                                                                                                                                                                                                                                                                                                    N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                    STKDFNLDLVSVSKKDSGASPRITSTSLCTPGCKTGALMGCNMKTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                544
558
771 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131
198
268
224
224
483
529
573
615
697
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                    HETERODIMER
                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transcripti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WD_REPEATS_REGION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       267
450
227
521
568
612
695
736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Phosphorylation; Wnt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83212 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18.9%;
                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                             sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      on regulation; Repressor; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WD 1.
WD 2.
WD 3.
WD 4.
WD 5.
WD 6.
WD 7.
WD 7.
PHOSPHORYLATION
PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLY/PRO-RICH.
CCN DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /FTId=VSP_007025.
R -> G (IN REF. 1).
W -> R (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 57.5;
Pred. No. 1
                                                                         CATALYTIC LINKED BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHOSPHORYLATION (BY Missing (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SER/PRO-RICH.
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                           (Enterokinase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F8263B8A418F757A
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                              1069
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                                                                                                                                                                                                                                                                                                                    update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17;
                                                                         A DISULI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             signaling
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
                                                                          DISULFIDE
                                                                                                       (BY SIMILARITY).
of 6-Lys-|-Ile-7 bond
                                                    protein (Probable)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BY
(BY
(BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                        22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                    CHAIN AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CBC2)
CBC2)
CBC2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                     Sadler J.E.;
                                                                          BOND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                          expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                 311
                                                                                                                                                                                                                                                                                                                                                                                                                                    48
                                                                          KB)
                                            S
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Sir and Paris

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PETAM: PP00431; CUB; 2.

PETAM: PP00431; CUB; 2.

PETAM: PP00629; MAM; 1.

PETAM: PP00629; MAM; 1.

PETAM: PP00629; SEA; 1.

PETAM: PP00330; SECR; 1.

PETAM: PP00330; SECR; 1.

PETAM: PP00330; SECR; 1.

PETAM: PP00030; MAMDOMAIN.

PRINTS; PR000261; LDLRECEPTOR.

PRINTS; PR000261; LDLA: 2.

SMART; SM00019; LDLA: 2.

SMART; SM00109; LDLA: 2.

SMART; SM00109; SEA; 1.

SMART; SM00200; SEA; 1.

SMART; SM00200; SEA; 1.

SMART; SM00200; SEA; 1.

SMART; SM00200; TYYD SPC; 1.

SMART; SM00200; TYYD SPC; 1.

PROSITE; PS001209; LDLRA 1; 2.

PROSITE; PS001209; LDLRA 1; 2.

PROSITE; PS50068; MAM; 1; 1.

PROSITE; PS50069; MAM; 1; 1.

PROSITE; PS50024; SEA; 1.

PROSITE; PS50024; SEA; 1.

PROSITE; PS50040; TRYPSIN DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001314; Chymotrypsin.
InterPro; IPR000859; CUB domain.
InterPro; IPR002172; LDL receptor A.
InterPro; IPR002098; MAM domain.
InterPro; IPR000082; SEA_domain.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001190; Srcr_receptor.
    DOMAIN
DO
                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U73378; AAB37317.1; -. HSSP; Q07954; 1CR8. MEROPS; S01.156; -. MGD; MGI:1197523; Prss7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Contains 1 SEA domain. SIMILARITY: Contains 1 SRCR domain. SIMILARITY: Contains 1 MAM domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PS00134;
PS00135;
      48
52
227
227
2387
569
686
830
830
830
830
830
688
688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LDLEA_1; 2.
LDLEA_2; 2.
MAM_1; 1.
MAM_2; 1.
SEA; 1.
SRCR_1; FALSE_NEG.
SRCR_2; 1.
SRCR_2; 1.
TRYPSIN_DOM; 1.
TRYPSIN_SER; 1.
TRYPSIN_SER; 1.
    1069
169
268
379
549
679
724
816
1069
874
925
1021
242
255
266
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CUB 2.

LIL-RECEPTOR CLASS A SRCR.

SEXING PROTEASE.

CHARGE RELAY SYSTEM (CHARGE RELAY SYSTEM (CHARGE RELAY SYSTEM (CHARGE RELAY SYSTEM (CHARGE RELAY SYSTEM (BY SIMILARITY.)

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.
                                                                                                                                                                                                                                                          SEA.
LDL-RECEPTOR CLASS A 1.
CUB 1.
MAM.
                                                                                                                                                                                                                                                                                                                                                                                      NON-CATALYTIC CHAIN (HEAVY CHAIN).
CATALYTIC CHAIN (LICHT CHAIN).
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hydrolase; Serine protease; Zymogen;
                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL).
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RESULT 1 Q93GH3 ID Q93G ID Q93G AC Q93G DT 01-D DT 01-D DT 01-M DE HYDS GN ERIS OS Bact OX NCBI RN [1] RN [1] RR SEQU RC STRA RA HOSE RT "A E RT "A E RT (put RT Cyut SUBM DR EMBI DR Matches Query Match Best Local : Hofemeister J.; "A subtilin-like gene cluster of Bacillus subtilis Al3 encodes (putative) lantibiotics, ericin A and ericin S."; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF233755; AAL15569.1; -. InterPro; IPR000446; Nisin. PRINTS; PR00324; NISIN. Q93GH3 PRELIMINARY; PRT; 56 AA. Q93GH3; 01-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Hypothetical 6.2 kDa protein. ERISB Bacillus subtilis. Bacteria; Firmicutes; NCBI_TaxID=1423; Hypothetical protein. SEQUENCE 56 AA; 6241 MW; STRAIN=A13; Stein T., Borchert S., Conrad B., Feesche J., Entian K.-D., SEQUENCE FROM N.A. σ . Similarity 29; Conserv DFNLDLVSVSKKDSGASPRITSTSLCTPGCKTGALMGCNMKTATCHCSIHVSK 57 DFDLDVVKVSKQDSKITPQWKSESVCTPGCVTGVLQTCFLQTITCNC--HISK Conservative 51.0%; Score 155; DB 2; Length 56; 54.7%; Pred. No. 8.2e-13; tive 10; Mismatches 12; Indels Bacillales; Bacillaceae; Bacillus. DEDEAB0892A1EBBA CRC64; two 56

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SEQUENCE 56 AA; 6195 MW; DI
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InterPro; IPR006078; Gallidermin.
InterPro; IPR006079; Lan dom.
Pfam; PF02052; Gallidermin; 1.
PRINTS; PR00323; GALLIDERMIN.
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Baba T., Takeuchi F., Kuroda M., Yuzawa
Nagai Y., Iwama N., Asano K., Naimi T.,
                                                                                                                                                                                                                                                       Complete proteome. SEQUENCE 47 AA;
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Bacteria; Firmicutes; Bacillales; Staphylococcus
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BSAA2 OR MW1765.
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EMBL; AF233755; AAL15567.1; ..
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"Genome and virulence determinants
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F., Kuroda M., Yuzawa H., Aoki K.-I., Ogr
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QBWUL3;
01-MAR-2002 (TrEMBLrel. 20, Cr
01-MAR-2002 (TrEMBLrel. 20, Li
01-MAR-2003 (TrEMBLrel. 23, L
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InterPro; IPR007091; LRR_RNinh.
InterPro; IPR003590; LRR_RNinh_sub.
Pfam; Pr00560; LRR; 3.
Pfam; Pr00560; LRR, RI; 1.
PR0SITE; PR50503; LRR_RI; 4.
Hypothetical protein.
SEQUENCE 456 AA; 49816 MW; 007B7;
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01-DEC-2001
01-DEC-2001
01-MAR-2003
                                                                                        Pfam; PF00008; EGF; 8.

PRINTS; PR00011; EGFLAMININ.

SMART; SM00180; EGF Lam; 4.

PROSITE; PS00022; EGF 1; 10.

PROSITE; PS01186; EGF 2; 10.

EGF-like domain; Laminin EGF-like domain.

SEQUENCE 567 AA; 60797 MW; CF2FB8CDEB
                                                                                                                                                                                                   Strausberg R.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC020198; AAH20198.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                           InterPro; IPR006209; EGF like.
InterPro; IPR002049; Laminin_EGF.
                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                              Similar to MEGF10 pr
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical RNH1.
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                       FISSUE=Muscle;
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BC010331; AAH10331.1; -.
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TSRCQ--CKNGAL--CNPITGACHCA 170
                      TSLCTPGCKTGALMGCNMKTATCHCS 52
                                                                                                                                                                                                                                                                                                                                                                                                                                             LSLASNELKDEGA--RILCESLLEPGCQLESLWIKTCSLTAASCPYFCSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LDLVSVSKKDSGASPRITSTSLCTPGCKTGAL--MGCNMKTATC--HCSI 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
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38.0%;
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53.8%;
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                                           Score 63; DB 4
Pred. No. 9.2;
1; Mismatches
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Last annotation updat
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                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                             CF2FB8CDEB7CF627 CRC64;
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InterPro; IPR006209; EGF like.
InterPro; IPR002049; Laminin_EGF.
IfterPro; IPR002049; Laminin_EGF.
IfterPro; IPR00011; EGF; 14.
PRINTS; PR00011; EGF; 14.
PRINTS; PR00012; EGF Lam; 6.
PROSITE; PS001022; EGF 1; 17.
PROSITE; PS01062; EGF 2; 17.
PROSITE; PS0106; EGF 2; 17.
PROSITE; PS0106; EGF 2; 17.
STANDARD PROSITE; PS01106; EGF 2; 17.
PROSITE; PS0106; EGF 2; 17.
PROSITE; PS0106; EGF 2; 17.
PROSITE; PS0106; EGF 3; 17.
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Q96KG7;
Q1-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9FKZ9;
                                                                                                                                 "Structural analysis of Arabidopsis thaliana chromosome 5. V. features of the regions of 1,381,565 bp covered by twenty one physically assigned Pl and TAC clones.";
DNA Res. 5:131-145(1998).
EMBL; AB010700; BAB08623.1; -.
InterPro; IPR006595; CTLH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
MEGF10 protein (Hypothetical protein KIAA1780).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2003 (TrEMBLrel. 23,
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01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2003 (TrEMBLrel. 23,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Hippocampus;
MEDLINE=21245130; PubMed=11347906;
                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                 Tabata S.;
                                                                                                                                                                                                                                                                                                    Kaneko
                                                                                                                                                                                                                                                                                                                       MEDLINE=98344145;
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                           SM00668;
CE 752 A
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Similarity
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                   20.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Brassicaceae;
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                     Score 62;
Pred. No.
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                                                                                           1FE23D5DC461AFC2 CRC64;
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                                        Length 752;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The genome sequence of Bifidobacterium longum reflects to the human gastrointestinal tract.";
Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
EMBL; AE014738; AAN24953.1; -
Hydrolasse; Complete proteome.
SEQUENCE 475 AA; 52701 MW; 2CF00D99BZF8C907 CRCK4.
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Q8G572;
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InterPro; IPR001313; Pumilio/Puf.
SEQUENCE 536 AA; 58248 MW; 40
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Bacteria; Actinobacteria;
Bifidobacteriaceae; Bifid
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DGT OR BL1148.
                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pessi G., Zwahlen M.-C., Desiere F., Pridmore R.D., Arigoni F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2003
01-MAR-2003
                                                                                                                                                                                                                                                                                                                       TISSUE=Lung;
                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
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                                              11 VSVSKKDSGASPRITSTSLCTPGCKTGALMGCNMKTATCH-CSIHV
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                                                                                               l Similarity
13; Conserv
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LSTNRTGSEMLQELLGFSPLKPLCRVWAALRSNLRTVACHRCGVHV
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                                                                                                 Conservative
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(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                        Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata;
                                                                                                                   20.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20.2%;
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Desiere F., Bork P., Delle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Actinobacteridae; Bifidobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 61.5; D
Pred. No. 12;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8;
                                                                                                 9
                                                                                                                        Score 61.5;
Pred. No. 1
                                                                                               Pred. No. 14;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                             DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 16;
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                                                                                                 23;
                                                                                                                                                                                                                                                                        databases
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                                                                                                                                                                                                CRC64;
                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                 Indels
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                                                                                                                                                  536;
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Burandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Bril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000
01-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CG12908 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9V5J7;
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Mammalia; I
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01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20196006; PubMed=10731132;
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Eutheria;
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llarity 28.3%;
Conservative
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Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          el. 23, Created)
el. 23, Last sequence update)
el. 23, Last annotation updat
KIAA2021 (Fragment).
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22,
23,
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a long cDNA clone
EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 61.5; D
Pred. No. 17;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pterygota;
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A Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,

A Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,

A Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,

A Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

A Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

A Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D...

A Perriera S., Frise E., Galle R.F., Garg N.S., George R.A.,

A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

A Pacleb J., Paraggas V., Park S., Patel S., Pfeifer B.,

A Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,

Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,

Milliams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;

"Sequencing of Drosophila melanogaster genome.";

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                          Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                FlyBase; FBgn0033509; CG12908.
InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR00181; EGF Ca.
InterPro; IPR006209; EGF_like.
InterPro; IPR006210; IEGF.
InterPro; IPR00033; Ldl_receptor_rep.
InterPro; IPR00386; Nidogen_ext.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [3]
SEQUENCE FROM N.A.
Matthews B.B., Bayraktaroglu L., Campuller S., Crosby M.A., Matthews B.B., Prochnik S.B., Smith C.D.,
Hradecky P., Huang Y., Kaminker J.S., Prochnik S.B., Smith C.D.,
Tupy J.L., Bergman C., Bermert D., Frise E., de Grey A., Harris N.,
Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.,
"Annotation of Drosophila melanogaster genome.";
"Annotation of Drosophila melanogaster genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weisenbach J.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
Zhong T.N., Zhong W., Zhou X., Smith H.O.,
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
                                                                                                                                                     PROSITE;
EGF-like
                                                                                                                                                                                                                   PROSITE; PROSITE;
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Pfam; PF00058; Idl recept b; 2.
SMART; SM00131; EFF; 11.
SMART; SM00135; LY; 4.
SMART; SM00539; NIDO; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (SEP-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FlyBase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE003830; AAF58809.
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                                                                                                                        domain.
1350
                                                                                                                                                                               PS00010; ASX_HYDROXYL;
PS01186; EGF_2; 9.
PS01187; EGF_CA; 1.
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D., Celniker S.E.,
d (MAR-2000) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FROM N.A.
                                                                                                                        A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murphy
                          20.1%;
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                                                                                                                           149081
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B., Murphy L.,
Score 61; DB Pred. No. 42; 3; Mismatches
                                                                                                                           Μ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL/GenBank/DDBJ databases
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                                                             5; Length 1350;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Campbell K., nith C.D., sr S.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rogers Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D.A.,
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Q924P4;
                                                                                                                                                                                                                                                                                                                                                                               Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Chawez C., Dorsett V., Dresnek D., Farfan D., Frise George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8T919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Mouse homolog of ribonuclease/angiogenesis inhibitor.", Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RNH1
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Stapleton M., Brokstein P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AT05602p.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                          Submitted (JAN-2002) to the EMBL/GenBank/DDBJ EMBL; AY075166; AAL68036.1; -.
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                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                Celniker S.;
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InterPro; IPR007091; LRR_RNinh.
InterPro; IPR003590; LRR_RNinh_
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1; SM00368; LRR_RI; 1.
[TE; PS50503; LRR_RI;
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                                                                                                                                                                          FBgn0035477;
773 AA; 8
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Pred. No. 18;
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                                                                                     DB 5; Length 773;
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        Indels
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RESULT OF COCK OF COCK
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Holt R.A., How, Honderson S.N.,
RA George R.A., Levis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Haris M.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Ffannkoch C., Baldwin D.,
RA Ballow R.M., Beau A., Baxendale J., Bayrakkaroglu L., Beasley E.M.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Gherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Perraz C., Ferriera S., Fleischmann W.,
RA Coslor K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Perraz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kull D., Lai Z.,
Lai Z., Lai Z., Lin Z., Lin Z., Lin Z., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K., Saunders R.D. C., Scheeler F., Shen H.,
RA Melson D.R., Nelson K., Saunders R.D. C., Scheeler F., Shen H.,
RA Melson D.R., Nelson K., Saunders R.D. C., Scheeler F., Shen H.,
RA Melson D.R., Weisser J.S., Zhan M., Shapa A.H., Wang X.,
RA Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Syirskas R., Tector C., Turner R., Jenson M., Stupski M.P., Smith T.,
RA Shen S. F., Saequence of Dros
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Q9VZK7;
01-MAY-2000 (TrEN
01-OCT-2002 (TrEN
01-MAR-2003 (TrEN
CG14982 protein.
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,

Celniker S.E., Adams M.D., Amanatides P.G., Brandon R.C., Rogers Y.,

Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Busam D.A.,

Carlson J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,

Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,

Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,

Ferriera S., Frise E., Galle R.F., Hostin D., Howland T.J.,

Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

Thegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,

McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ephydroidea; Dro
NCBI_TaxID=7227;
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CG14982
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophilidae; Drosophila
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RESULT 15
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                 A Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
A Alvarenga R., Alves L.M.C., Arruda P., Baia G.S., Baptista C.S.,
A Alvarenga R., Alves L.M.C., Arruda P., Baia G.S., Baptista C.S.,
A Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
A Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
A Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
A Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
A Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
A Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
A Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
A Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Kitajima J.P.,
A Hopel, J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
A Lemos E.G.M., Lemos M.V.F., Lopes C.R., Machado J.A.,
A Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
A Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
A Menck C.F.M., Miracca B.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.I.T.O., Netto L.E.S.,
A Mania A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
B Dereira G. N. Descripa H. A., Paris A.,
B Dereira G. R. Descripa H. A., Paris A.,
B Dereira G. R. Descripa H. A., Paris A.,
B Dereira G. R. Descripa H. A., Paris A.,
B Dereira G. R. Descripa H. A., Paris A.,
B Descripa G. D. Descripa H. A., Paris A.,
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B Descripa G. D. Descripa H. A., Paris A.,
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B Descripa G. D. Descripa H. A., Paris A.,
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B Descripa G. D. Descripa H. A., Paris A.,
B Descripa G. D. Descripa H. A., Paris A.,
B Descripa G. D. Descripa H. A., Paris A.,
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B Descripa G. D., Paris A., Pander D. D., Paris A.,
B Descripa G. D., Paris A., Paris A.,
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Best Local S
Matches 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE003479; AAF47814.2; -. FlyBase; FBgn0035477; CG14982. SEQUENCE 773 AA; 84832 MW: EIRCRAFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical XF2284.
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Adams M.D., Celniker S.E.,
Submitted (MAR-2000) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20365717; PubMed=10910347;
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01-MAR-2002
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16; Conser
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   G.A.G., Pereira H.A. Jr.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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Prochnik S.E., Smit
lson J.W., Celniker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 5;
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"The genome sequence of the plant pathogen Xylella fastidiosa."; Nature 406:151-159(2000).
                                                                                                                                  EMBL; AE004040; AAF85083.1; -. Hypothetical protein; Complete SEQUENCE 78 AA; 8776 MW; 10
 5
                                 23
                                                                  14;
                                                                                  Similarity
RPDAVSVLTPGCKQAGATLLTLRVRATLYCSTHI 48
                             RITSTSLCTPGCK-TGALMGCNMKTATCHCSIHV
                                                                  Conservative
                                                                                19.6%;
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Search completed: January 12, 2004, 14:25:56 Job time : 56 secs

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Minimum
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Compugen Ltd
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. 675 643 604 518 518 503.2 440 4144 410.4 400.4 400.4 400.4 380.3 380.3 358.4 358.4 358.4 358.4 358.4 358.4 300.2 3 765.4 765.4 750.2 687.4 77.8 77.8 77.8 77.8 77.8 60.6 Match 24.6 22.7 11.1 10.7 10.7 10.4 10.1 10.1 10.1 10.1 10.1 46.7 46.7 46.7 39.1 249050 349980 349980 110000 Length 66993 1446 BB STRNISA AXX80058 AXX002984 AXX002983 A76046 AR030515 AR119687 AXX415244 AXX415244 AXX413559 AL596165 AXX417038 AXX417038 AXX417038 AXX417038 AXX417038 AXX417038 AXX417038 AXX417038 AR228336 AR228338 AR228339 AR228340 LACNISABTC AX002982 LACNISINA BD166172 STRSPAN AF465351 AF420259 LLNISGEN AR228341 LACSPAN LLNISI M24527 Streptococc AX280058 Sequence AX002984 Sequence AX002983 Sequence AX002983 Sequence AX602983 Sequence AX61515 Sequence AR119687 Sequence AX415244 Sequence AX415244 Sequence AX413559 Sequence AX417041 Sequence M65089 Lactococcus Y13384 Lactococcus A76045 Sequence 1 AX322999 Sequence D10768 L.lactis mu M27277 Lactococcus X61144 L.lactis ni A30280 L.lactis Ni A30280 L.lactis Ni A30280 Sequence 1 A3037 Sequence 1 A51037 Sequence 1 A51037 Sequence 1 A528337 Sequence AR228336 Sequence AR228338 Sequence AR228339 Sequence AR228339 Sequence AR228339 Sequence AX002982 Sequence M79445 L.lactis OR BD166172 Leader se I09640 Sequence 3 AB083093 Lactococc Z18947 Lactococcus AR228341 Sequence J04057 S.lactis an AF465351 Lactococc AF420259 Lactococc D00696 Lactococcus X68307 L.lactis ge Description AC138074 Homo sap: L16226 Lactococcus

ALIGNMENTS

TITLE	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	STRSPAN	RESULT 1
Structure, expression, and evolution of a gene encoding the precursor of nisin, a small protein antibiotic	Buchman, G.W., Baneriee, S. and Hansen, J.N.	1 (bases 1 to 767)	Lactococcus.	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;	Lactococcus lactis	Lactococcus lactis	nisin; small protein antibiotic.	J04057.1 GI:153816	J04057	S.lactis antibiotic nisin (spaN) gene, complete cds.	STRSPAN 767 bp DNA linear BCT 15-FEB-1996		

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Direct Submission
Submitted (05-JAN-2002) Department of Dairy and Submitted (05-JAN-2002) Department of Dairy and Royal Veterinary and Agricultural University of Rolighedsvej 30, Frederiksberg C 1958, Denmark
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   from Chr. Hansen
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                       TAGCTAATCCTAAACTCTATGATGTTATGCAGAAATATAATGCTGGT
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                                                                                     CTCAACCGTTTTTAGTAAGAAATACAATTTTATCTCCAAACGATAAACGGAGTTTTACTG
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                                                                                                                                                                                                     TTGCTAAATAGCTTATAAAAATAAAGAGAGAAAAAACATGATAAAAAGTTCATTTAAAG
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INSSELEEVNIKYTNVYQIISEFCENDYQKYEDICETVTLCYGDEYRELSEQYLGSLI
VNHYLISNLQKDLLSDFSWNTFLTKVDEAIDEDKKYJIFLGXSDEIGGGI
EKLKEIYQEMSQILENDNYIQIDLISDSEINFDVKQKQQLEHLAEFLGNTTKSVKRTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l (bases 1 to 1575)
Lee, K.-H., An,J.-Y., Yun,H.-D., Lee,H.-J.,
Chung,D.-K., Lee,J.-H. and Kim,J.-H.
Characterization of a nisin-producing Lacto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene, partial cds.
AF420259
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Bacteria; Fírmicutes; Lactobacillales;
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      AATAGAAACATTAACAAATCTAAAACAGTCTTAATTCTATCTTGAGAAAGTATTGGTAAT
                                                                                                            AGTTGACGAATATTTAATAATTTTAATATATCTTGATTTTCTAGTTCCTGAATAATATA
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INSSELEEVNIKYTNYYQIISEF"
1198 c 257 g 530 t
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and NisB (nisB)
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Lactococcus lactis
Bacteria; Firmicutes; Lactobacillales;
                                                                                                                                                                                    Nutritional Science Laboratory Morinaga Milk Industry Co., Ltd. 1-83, 5 Higashihara
                                                                                                                                                                                                                                                        These data kindly submitted in
                                                                                                                                                                                                                                                                           Unpublished
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                                                                                                                                                                    Kanagawa 228
                                                                                                                    81-462-52-3047
81-462-52-3055
 /db_xref="taxon:1358"
71. .109
                                                                                                    Location/Qualifiers
                                                              organism="Lactococcus lactis"
                                                                                                                                                                                                                                                                                                                                                                                                         GI:216734
                                  mol_type="genomic DNA"
strain="NCDO497"
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                                                                                                    AGTTGACGAATATTTAATATTTATTAATATCTTGATTTTCTAGTTCCTGAATAATATA
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QLLLANPKLYDVMQKYNAGLLKKKRVKKLFESIYKYYKRSYLRS"
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TY1PTKEGTLYLANVILVESRKIVGWSRSKRYGDKLVRDCFLQAKGKEHPQPGLIVHT
DQGSQYTSSRYQSTLRQVGAQSSMSRKGNPYDNAMMESFYKTLKRELINDAHFETRAE
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/note="ORF3"
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                                                                           Direct Submission
Direct Submission
Submitted (07-SEP-1992) G. Engelke, Inst. fuer Mikrobiologie,
Submitted (07-SEP-1992) Theodor-Stern-Kai 7, Haus 75A, 6
                                                                                                                                                                                           Engelke, G., Gutowski-Eckel, Z., Hammelmann, M. and Entian, K.D. Biosynthesis of the lantibiotic nisin: genomic organization membrane localization of the NisB protein Appl. Environ. Microbiol. 58 (11), 3730-3743 (1992)
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X68307.1 GI:44040
biosynthetic enzyme; lantibiotic; nisZ
Lactococcus lactis
Lactococcus lactis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGATACAATGATTTCGTTCGAAGGAACTACAAAATAAATTATAAGGAGGCACTCAAAATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGGATAGTATTTTGTTAGTTCAGACATGGATACTATCCTATTTTTATAAGTTATTTAGGG
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                                                                                                                                                                                                                                                                                                                                                                          lactis genes for nisin
                                                                                                                                                 (bases 1 to 7500)
                                                                                                                                                                                                                                                    (bases 1 to 7500)
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                                                          Location/Qualifiers
                                                                          70, FRG
                                              .7500
                                                                                                                                                                                                                                                                                                                                                                          7500
and
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biosynthetic enzymes.
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BASE COUNT
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                                                                                                                                                                                                                                                                                                                          TGTAACATGAAAACAGCAACTTGTCATTGTAGTATTCACGTAAGCAAATAACCAAATCAA
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FFKKASIYILDEPSAALDPVAEKEI FDYFVALSENNI SI FI SHSLNAARKANKI VVMK
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99.5%;
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Pred. No. 6.1e-120;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 7610)
Immonen,T., Ye,S., Ra,R., Qiao,M., Paulin,L. and Sari
The codon usage of the nisz operon in Lactococcus lac
suggests a non-lactococcal origin of the conjugative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 3055)
Engelke,G., Gutowski-Eckel,Z., Hammelmann,M. and Entian,K.D.
Biosynthesis of the lantibiotic nisin: genomic organization
membrane localization of the NisB protein
Appl. Environ. Microbiol. 58 (11), 3730-3743 (1992)
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gene; nisZ gene.
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239. .412
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University of Helsinki,
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DIVGNUNLGGASGRFSALSPELTSYHRTIVDSVERENENKEITSCETYPLPENIRHAN
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/product="WisP protein"
/protein_id="CAA79466.1"
/db_xref="GI:581294"
/db_xref="GI:581294"
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NAILSSTEGSTTDSINLGEQSTAVKSTTRTELDVTGAAKTLLQTSAVQKEMKVSLQET
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DTTVSDEELGEYQDVLAEVRVFDSVSGKSIÞRSEWGRIDKDGSNSKQSRTEWDYGEIH
SIRGKSLTEAFAVEINDDFKLATKVGN"
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7287. .>7610
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/citation=[1]
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Gasson, M.J. and Dodd, H.M.
Production of variant nisin
Patent: US 6448034-A 29 10-SEP-2002;
Location/Qualifiers
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Sequence
AR228341
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Unclassified.
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                                                                                                       TATTCACGTAAGCAAATAACCAAATCAAAGGATAGTATTTTGTTAGTTCAGACATGGATA
                                                                                                                                                                                                                                                                                           CGGTTGTAAAACAGGAGCTCTGATGGGTTGTAACATGAAAACAGCAACTTGTCATTGTAG
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 AAATATAATGCTGGT
                     AAATATAATGCTGGT 767
                                                                  AATAAAGTTTTTTTGGAACAGTTACTACTAGCTAATCCTAAACTCTATGATGTTATGCAG
                                                                                                                                                  AAAAACATGATAAAAAGTTCATTTAAAGCTCAACCGTTTTTAGTAAGAAATACAATTTTA
                                                                                                                                                                                 CTATCCTATTTTATAAGTTATTTAGGGTTGCTAAATAGCTTATAAAAAATAAGAGAGGA
                                                                                                                                                                                                                               TATTCACGTAAGCAAATAACCAAATCAAAGGATAGTATTTTGTTAGTTCAGACATGGATA
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                                                                                          AAAAACATGATAAAAAGTTCATTTAAAGCTCAACCGTTTTTAGTAAGAAATACAATTTTA
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29 from patent US 6448034.
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100.0%; Pred. No. 5.4e-107;
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Kuipers,O.P., Beerthuyzen,M.M., Siezen,R.J. and De Vos,W.M. Characterization of the nisin gene cluster nisABTCIPR of Lactococcus lactis. Requirement of expression of the nisA genes for development of immunity

Eur. J. Biochem. 216 (1), 281-291 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sub_species lactis) DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lactococcus lactis
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translocator protein.
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                                          LDDYKDKĒ I EKŸGVDQEVQI TELFDSTFGI GA PYNYNHĒRND FYESEPSTLYYSEEER EKYLSMYVEAVKHHVI INLDILESHYQKMDLEKKSELQELEIFLILAKEYEKDI FILG DI VGINNILGGASGRF SALS PELTS YHRT I VDS VERENENKE I TSCEI VFLPENI RHAN VMHTSIMRRKVLPĒTSTSHEVLLINI Y I GI DEKEKFYARDI STQEVLKFY I TSMYN KTLFSNELFLYEI SLDDKFGNLPWELI YRDFDY I PRLVFDE I VI SPAKWKI WGRDVN SKMTLFBLI QEKEFY I VNGDNKYVLSQEN PLOMEI LESAI KKSSKRKDF I ELQE YFEDENI I INKGEKGR VADVVVPĒ I RTRALGNIGRAF KKSVEKRE KELFPNEWLYL KLYI SI NRQNEFLLSYLDI QKI VANLGGNLFELRYTD FKH YECSDLFLAYGS I LEILKRSRKNEIMSTĒDI SI VDQEVERYGGFDTLELSEAI FCADSKI I PNLLITLI KD TNNDWKVDDVSILVNYLYLKOFFQNDNKKI LNFLINLVS PKKVKENNNEKI EHYLKLIK TNNDWKVDDVSILVNYLYLKOFFQNDNKKI LNFLINLVS PKKVKENNNEKI EHYLKLIK
DKEKLIYYTLQRLFVSEEYMK"
                                                                                                                                                                                                                                                                                     KKSQYKLMGKTTKGIRLDTQWLIRLVHKMEVDFSKKLSFTRNNANYKGDRVFQVYT
INSSELEEVNIKYTHVYQIISFCENDYKYEDICETYTLCYGDEYRELSEQYLGSLI
VNHYLISHLQKDLLSDFSWNTFLTKVEAIDEDKKYIIPLKKVOKFIQEYSEIBIJGED
EKLKEIYQEMSQILENDNYIQIDLISDSEINFDVKQKQQLEHLAEFLGNTTKSVRRTY
                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="AAA25190.1"
/db_xref="GI:400367"
/tzanslation="MIKSSFKAQPFLVRNTILSPNDKRSFTBYTQVIETVSKNKVFLB
QLLLANPKLYDVMQKYNAGLLKKKRVKKLFESIYKYYKRSYLRSTPFGLFSETSIGVF
                         VNNLGDQ1FYDKNFKELKHA1KNLFLKM1AQDFELQKVYS11DS11HVHNNRL1G1ER
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/label=ORF
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/strain="NIZO R5"
/sub_species="lactis"
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/transl_table=
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/protein_id="AAA25189.1"
/db_xref="GI:400366"
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ACAATGATTTCGTTCGAAGGAACTACAAAATAAATTATAAGGAGGCACTCAAAATGAGTA 180
                                 ACAATGATTTCGTTCGAAGGAACTACAAAATAAATTATAAGGAGGCACTCAAAATGAGTA 304
                                                                                                       TTATTGTCGATAACGCGAGCATAATAAACGGCTCTGATTAAATTCTGAAGTTTGTTAGAT
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/db_xref="G1:400368"
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SLFFIGTMNIGVAILLLIVPVLSLVLFILVATAVKQLEFILOWQRASSERETMYIVYLLTHD
FSFKEIKLNNISNYFIHKFGKLEKKGFINQDLAIARKKTYFNIFLDFILMLINILTIFA
MILSVRAGKLLIGNLVSLIQAISKINTYSQTMIQNIYIIYNTSLFMEQLFEFLKRESV
VHKKIEDTEICNQHIGTVKVINLSVLFNESHAFLKNINLSFEKGELTAIVGKNGSGK
STLVKIISGLVQPTMGIIQYDAISKINTYSQTMIQNISVLFQDFVXSLTTRENIGLS
DLSSQWEDEKIIKVLDNLGLDFLKTNNQYVLDTQLMWFQEGHQLSGGQWQKIALART
FFKKASIYILDEPSAALDPVLEKEIFDYFVALSENNISIFISHSLNAARKANKIVVMK
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                                                                                                                                                                                                                                                                                                /translation="MRRYLILIVALIGITGLSGCYQTSHKKVRFDEGSYTNFIYDNKS YFYTDKEIPQENVNNSKVKFYKLLIVDMKSEKLLSSSNKNSVTLVLNNIYEASDKSLC MGINDRYYKILPESDKGAVKALRLQNFDVTSDISDDNFVIDKNDSRKIDYMGNIYSIS DTTVSDEELGEYQDVLALEVRVFDSVSGKSIPRSEMGRIDKDGSNSKQSRTEMDYGEIH SIRGKSLTEAFAVEINDDFKLATKVGN"

9 13 c 1374 g 2407 t
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/gene="nisI"
/note="encodes a
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5242. .6486
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                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAA25193.1"
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/transl_table=11
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Best Local Similarity Matches 643; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                               Performance enhancement
Patent: WO 9941978-A 1 26-AUG-1999;
FLANAGAN ALISON JOHNSTONE (GB); ROLPH TIMOTHY PETER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lactobacillus delbrueckii subsp. lactis
Lactobacillus delbrueckii subsp. lactis
Bacteria; Firmicutes; Lactobacillales;
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Sequence 1 from Patent WO9941978.
AX002982
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                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/sub_species="lactis"
/db_xref="taxon:29397"
/note="NIZO R5"
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                                                                                                                                                                                                                                                                                                                                                               organism="Lactobacillus delbrueckii subsp.
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Original
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                                                                                                                                                                                                                                             Lactococcus lactis
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/organism="Lactococcus lactis"
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/mb_ref="taxon:1358"
625._.2521
/gene="nisin"
625._.1386
                                                                                             source text: Lactococcus
Location/Qualifiers
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(nisin) g
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and ORF3 (nisin)
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                                       AGGATAGTATTTTGTTAGTTCAGACATGGATACTATCCTATTTTTATAAGTTATTTAGGG
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Mintrkvgklihnglyakgsrykykhynkgaslskrinlinglykatarprkvmlgdm
Tylptkegtilavridyeskrivgmskskrydkurdptloacgkehpqpglijht
DQGSQYTSSRYQSTLRQVGAQSSMSRKGNPYDNAMMESFYKTLKRELINDAHFETRAE
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/db_xref="GI:551876"
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/translation="MSTKDFNLDLVSVSKKDSGASPRITSISLCTPGCKTGALMGCNM
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Pred. No. 1.1e-94;
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polypeptides in bacteria, and gene therefor
Patent: JP 2002191383-A 2 09-JUL-2002;
UNIVERSITY OF MARYLAND
OS Bacillus subtilis
pN JP 2002191383-A/2
pD 09-JUL-2002
PF 08-NOV-2001 JP 2001343857
PF 08-NOV-2001 JP 2001343857
PF 08-NOV-2001 JP 2001343857
PF 08-NOV-2001 JP 201343857
PR 05-JUL-1988 US 214959
PI NORMAN J HANSEN
PC C12N15/09,C07K14/195,C12N15/00
CC Leader sequence inducing a post-translational
CC Leader sequence inducing a post-translational
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FH Key Location/Qualifiers
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BD166172
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                               AGTACAAAAGATTTTAACTTGGATTTGGTATCTGTTTCGAAGAAGATTCAGGTGCATCA
                                                                                         AGATACAATGATTTCGTTCGAAGGAACTACAAAATAAATTATAAGGAGGCACTCAAAATG
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
74 c 89 g 168
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                                                                            TGTAACATGAAAACCAGCAACTTGTCATTGTAGTATTCACGTAAGCAAATAACCAAATCAA
                                                                                           TGTAACATGAAAACCAGCAACTTGTCATTGTAGTATTCACGTAAGCAAATAACCAAATCAA
                                                                                                                                         CCACGCATTACAAGTATTTCGCTATGTACACCCGGTTGTAAAACAGGAGCTCTGATGGGT
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                                                                                                                                                                  BASE COUNT
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Best Local Similarity
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Submitted (00-APR-2002) Sang-Hee Park, Tokyo University, Laboratory of Veterinary Public Health; Bunkyouku yayoi 1-1-1, Tokyo 113-8657, Japan (E-mail:park)hee@hotmail.com, Tel:81-3-5841-5476,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nisin B,
AB083093
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Lactococcus lactis subsp. lactis
Bacteria; Firmicutes; Lactobacillales;
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Park, S.H.
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Identification and Characteristics of Nisin Z-Producing Lactococcus
lactis subsp. lactis Isolated from Kimchi
"Lurr Microbiol. 46 (5), 385-388 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   actococcus.
                        TGGATTTGGTATCTGTTTCGAAGAAAGATTCAGGTGCATCACCACGCATTACAAGTATTT
                                                                GAAGGAACTACAAAATAAATTATAAGGAGGCACTCAAAATGAGTACAAAAGATTTTAACT
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QLLLANPKLYNVMQKYNAGLLKKKKNFESIYKYYKRSYLRSTPFGLFSETSIGVF
SKSSQYKLMGKTTKGIRLDTQWLIKLKLYHKMEVDFSKKLSFTRNNANYKFGDRVFQVY"
3 99 c 141 g 253 t
                                                                                                                                                                                                                   /product="nisin B"
/protein_id="BAC20310.1"
/db_xref="GI:23496478"
                                                                                                                                                                                                                                                                                                                                      KTATCNCSIHVSK"
                                                                                                                                                                                                                                                         /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                     /gene="nisB"
                                                                                                                                                                                                                                                                                                                                                 'protein_id="BAC20309.1"
'db_xref="GI:23496477"
'translation="MSTKDFNLDLVSVSKKDSGASPRITSISLCTPGCKTGALMGCNM
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/transī_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /isolation_source="Kimchi"
/sub_species="lactis"
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Steen,M.T., Chung,Y.J. and Hansen,J.N.
Characterization of the nisin gene as part of a polycistronic operon in the chromosome of Lactococcus lactis ATCC 11454
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Lactococcus lactis nisin and ORF B, 5' end.
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Bacteria; Firmicutes; Lactobacillales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source text: Lactococcus
Location/Qualifiers
                                                                                                                                                               KTATCHCSIHVSK"
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/db_xref="GI:149449"
                                                                                                                                                                                                   /codon_start=1
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/db_xref="GI:149448"
                                                             codon_start=1/transl_table=
                                                                                                                rpt_type=inverted
                                                                                                                                                                                    translation="MSTKDFNLDLVSVSKKDSGASPRITSISLCTPGCKTGALMGCNM/
                                                                                                                                                                                                                                                                                                                            gene="nicin"
                                                                                                                                                                                                                                                                                                                                                                                       mol_type="genomic DNA"
db_xref="taxon:1358"
                                                                                                                                                                                                                                                                                        gene="nicin"
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RESULT 15
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                                                                                                            TACTAGCTAATCCTAAACTCTATGATGTTATGCAGAAATATAATGCTGGT 767
                                                                                                                                                                                                                                                                                                                                                                                   GGGTTGCTAAATAGCTTATAAAAATAAAGAGAGGAAAAAACATGATAAAAAGTTCATTTA 597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGTTGTAACATGAAAACAGCAACTTGTCATTGTAGTATTCACGTAAGCAAATAACCAAAT 477
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LDDYKOKFIEKYGVDQEYQITELFDSTFGIGAFVNYNHFRNDFYSEBSTLYSSEER
EKYLSMYVEAKUNHVILUDDLESHYQXOMDLEKKSELQGLELFINLAKEYEKDIFILG
DIVGNNLIGGASGRFSALSPELTSYHRTIVDSVERENENEITSCEIVFLJENIRHAN
VMHTSIMRRKYLJFFTSTSHNEVLLTNIYIGIDEKEKYYARDISTQEVLKFYITSMYN
KTLFSNELRFLYEISLDDKFGNLFMELIYNDJDYIFRLYDDIVISQENKKTIMGRDVN
KTHSNELRFLYEISLDDKFGNLFMELIYNDJYIFRLYDDIVISQENKKTIMGRDVN
SKMTIRELIQSKEIFKEFYINNGDNKVYLSQENFLDMEILESAIKKSSKRKDFIELGE
YFEDENIINKGEKGRVADVVVPFIRTRALGNEGRAFIBEKRVSVERREKLFFNEWLYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="AAA73040.1"
/db_xref="GI:149450"
/translation="MDEVKEF"
383 c 590 g 1053
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INSSELEEVNIKYTNVYQIISEFCENDYQKYEDICETVTLCYGDEYRELSEQYLGSLI
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QLLLANPKLYDVMQKYNAGLLKKKRVKKLFESIYKYYKRSYLRSTPFGLFSETSIGVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KLYISINRQNEFLLSYLPDIQKIVANLGGNLFFLRYTDPKPHIRLRIKCSDLFLAYGS
ILEILKRSRKNRIMSTFDISIYDQEVERYGGFDTLELSEAIFVPILKLFQICLH"
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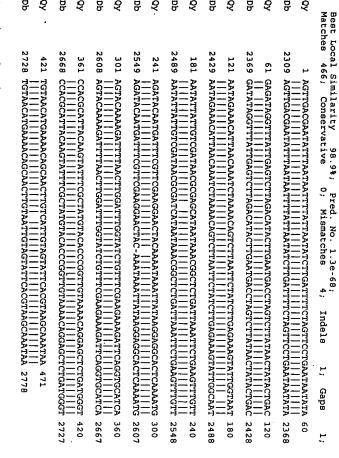
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REFERENCE
AUTHORS
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AUTHORS
TITLE
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Query Match
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Direct Submission
Submitted (27-MAY-1997) T. Immonen, Institute Of Biotechnology,
Submitted (1, Viikinkaari 9, P.O.Box 56, 00014 University Of
Helsinki, FINLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lactococcus lactis subsp. lactis
Lactococcus lactis subsp. lactis
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nisin Z; NisZ gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immonen, T
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                                                            1020
                                                                            /translation="MSTKDFNLDLVSVSKKDSGASPRITSISLCTPGCKTGALMGCNMKTATCNCSIHVSK"
                                                                                                                                                                                                                                                                          2605
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/translation="MDNSKLFGEAANEEQLLKNDYRKYCGENMDIYYNVAICEHAGEC
VRGNPLVFEYSRKPWIIPDNGDVASNQSVINRCPSGALKYLAKEKN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (932.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MPFWSTKIFGEGEKLMNIIERENLFELLSDKGEIIGEMAYMPMN
NSIIITHTGVSLDYRGQGLAKKLVLAGIQKARREQLKLGATCPYAVKYFREHKEELTD
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NEGFLITAVGFFFLGIIALGISQSNGVFELAGSKVNRIYAYIFTILLYLVIGFFFALPR
LATTISFEIGISPFLSHELQAFLALFSILFFGTAWFLSR"
complement (660. .977)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="homologous to branched chain transporters of LIV-II class" /protein_id="CAA73811.1" /db_xref="GI:3157417"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (<1. .423)
                                                                                                                                                                                                                2605. .2778
/gene="nisZ"
                                                                                                                                                                                                                                                                                                                                             /product="YjdI-like protein"
/protein_id="CAA73813.1"
/db_xref="GI:3157419"
                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
/transl_table=11
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                                                                                                                                                       /product="nisin Z"
                                                                                                                                                                                                                                    /gene="nisZ"
2605. .2778
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/clone="pLEB506"
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                                                                                                                 protein_id="CAA73814.1"
db_xref="GI:3157420"
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Length 2778;
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Searth completed: January 12, 2004, 12:57:03 Job time: 3040 BECB

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Title:
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                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                  410.4
410.4
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                                                                                                                                                                                                                                      Score
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Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                      Match
                                                                                                                                                                                                                                                                   Query
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/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:
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/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:
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46.6	46.8	46.8	46.8	47	47.2	48	48	48	48	48	48.2		48.4	•	48.4	•	٠	50.4	•	52.2	52.8	٠	٠	٠	•	77.8	٠		77.8	80	81.8	84.8	02.	19.	319.4	319.4
6.1	6.1	6.1	6.1	6.1	6.2		6.3	6.3	6.3	6.3	6.3	6.3	6.3	6.3	6.3	6.3	6.4	6.6	6.7	6.8	٠	7.0	7.1	7.4	7.6	10.1	0.1	0.1	10.1	0.4	0.7	-	6.4	1.6	41.6	41.6
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Nisin A; nisA gene; antimicrobial; preservative; antibiotic; lantibiotic; protein engineering; ds. Nisin nisABTCIP gene cluster 01-AUG-1996 (first entry) AAT29660; AAT29660 standard; DNA; 7454 BP.

ALIGNMENTS

ARESULT 1
AAT29660
ID AAT2
XX AAT2
XX AAT2
XX Nisi
DE Nisi
XX Nisi
XX Lact
XX Lact
XX Lact
XX FT repe
FT repe
FT -35FT -10FT RBS
FT CDS -10_signal -35_signal repeat_unit repeat_unit Lactococcus lactis strain NIZO R5. /label= p1-35 152..157 /*tar-/*tag= d /label= p1-10 191..197 /*tag= 0 Location/Qualifiers *tag= rpt_type= INVERTED *tag= type= INVERTED

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The gene cluster nisABTCIPRK (see AAT29660 and AAT29661) of Lactococcus lactis includes the nisA gene coding for pre-nisin A (AAR95267, see also AAR95263) and the genes for nisin modification, secretion and immunity. nisB (AAR95268) and nisC (AAR95270) are believed to be involved in reactions that modify pre-nisin; nisT (AAR95269) is similar to a transport ATPase and is involved in translocation of nisin out of the cell; nisI (AAR95271) is involved in immunity to nisin. Replacement of the natural, chromosomal copy of the nisA gene with a variant nisA gene allows prodn. of high levels of nisin A variants in Lactococcus lactis hosts.
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                                                                                                                                                 Disclosure; Fig 7; 69pp; English.
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/1abel= nisB
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5260.5267
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                                                                                                                                                                                   does not contain natural nish nish gene, and genes for nisin
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Sequence

7454

2741 A;

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1376 G;

2417

T; 0

other;

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AC AAX8
AC AAX8
AC AAX8
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XX Nisi
XX Nisi
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                                                                                                                                Nisin gene region of Lactobacillus lactis.
                                                                                                                                                         09-NOV-1999
                                                                                                                                                                                 AAX87792;
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                                                          Lactobacillus lactis.
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                                                                               This is the nisin gene region of Lactobacillus lactis NIZO R5, including the nis A, nis B, nis T, nic C and nis I genes that respectively code for nisins A, B, T, C and I (see AAY0665-69). The invention relates to methods of enhancing performance in an animal by administering a bacterium capable of expressing a performance enhancing polypeptide such as nisin A or nisin Z. The enhanced performance results in improved growth rates and feed conversion efficiencies. The bacterium, which may be genetically modified to express the performance enhancing polypeptide, is sufficient to express the performance enhancing polypeptide, is a embryo or neonatal animal. If the polypeptide is nisin, it may also inhibit ruminal methane, decrease acetate to propionate ratios and prevent amino acid deamination. Administration of an appropriate bacterium which may act as a probjectic may also help control enteric pathogens in poultry. The polypeptide is produced continuously in the gut, maintaining a constant level. The protein is eventually degraded, leaving no residues in the meat.
                                        Query Match
Best Local Similarity
Matches 643; Conserv
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                                                                              Sequence
                                                                                                                                                                                                                                                           Disclosure; Page 55-57; 79pp; English.
                                                                                                                                                                                                                                                                            Novel performance enhancing method resulting in improved growth rates and feed conversion efficiencies in animals
                                                                                                                                                                                                                                                                                                      P-PSDB; AAY06665,
                                                                                                                                                                                                                                                                                                                                 Flanagan AJ,
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                                                                                                                                                                                                                                                                                                                                                  (PFIZ ) PFIZER INC. (PFIZ ) PFIZER LTD.
                                                                                                                                                                                                                                                                                                                1999-527402/44.
      7423
                                           Conservative
                                                                              BP; 2729 A; 913 C; 1374 G; 2407 T; 0 other;
                                                                                                                                                                                                                                                                                                                                 Haxell MA,
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3435...
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455..3436
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Nisin precursor peptide; peptide leader fragment; peptide leader sequence; post-translational modification;
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                                                                                                                                                                                                                                                                                                                                                         Streptococcus
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 It contains a gene leader fragment encoding peptide leader sequence which induce post-translational modification (PTM) of amino acids Cys, Ser and Thr. The nisin gene was found in S. lactis using 20mer probe (see FT tag f). A DNA fragment is prepared encoding a precursor polypeptide attached to a leader fragment, this is then inserted into an expression vehicle to express and modify the precursor polypeptide. Modified proteins containing dehydroalanine and dehydrobutyrine which can covalently bind to targets, and adhesives for specific substrates can be designed. Tag b is claimed in the patent in claim 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 518 BP; 187 A; 74 C; 89 G; 168 T; 0 other;
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P-PSDB; AAR05238.
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including post-translational modification of polypeptide(s)
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                                                Nisin is a highly modified peptide antibiotic produced by certain bacteria e.g. strains of Lactococcus lactis. It has efficient antimicrobial activity against a wide range of Gram positive bacteria which are food pathogens or spoilage organisms. The genes involved in nisin maturation can be used to transform other microbes which are unable to secrete the natural nisk nisin. These organisms can however modify nish and translocate it out of the cell. This provides an effective means of producing variant nishs which are useful as antimicrobial agents in conditions of high pH where natural nish is ring-opened and loses its antimicrobial properties. (Updated on 25-MAR-2003 to correct PN field.)
Sequence 448
                                                                                                                                                                                                                                                                                                                                                                                                                                      New organisms able to express genes for nisin maturation, native pre-nisin - useful for producing variant nisin(s) antimicrobial use in food industry
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/note= "Inverted repeat."
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/label= nisB gene
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  80 G; 137 T; 0 other;
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Query Match
Best Local Similarity
Matches 448; Conserv

58.4%; Score 448; ilarity 100.0%; Pred. No. Conservative 0; Mismatch

Mismatches

<u>0</u>

Gaps

0

4.4e-81;

DB 14; Length 448; Indels

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ARESULT 5
AAT2961
AAT291
IID AAT27
XX AAT2
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XX Nisi
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XX ET -35-
FT -10
FT -10
FT -10
FT 17-
PN EP71
PN E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nisin Z; lactococcus; lactic acid bacterium; promoter; membrane protein; antimicrobial peptide; nisin A; cell lysis; enzyme; fermented foodstuff; extracellular protein; dairy product; cheese; yoghurt; inducer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nisin A promoter fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT29611 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-JAN-1997
  WPI; 1996-252838/26
                                                  De Vos WM,
                                                                                                                                                    18-NOV-1994;
18-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lactococcus lactis
                                                                                                                                                                                                                                17-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -10_signal
                                                                                                    (NIZO-) NIZO STICHTING NEDERLANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -35_signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAAATAAATTATAAGGAGGCACTCAAAATGAGTACAAAAGATTTTAACTTGGATTTGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAATAAATTATAAGGAGGCACTCAAAATGAGTACAAAAGATTTTAACTTGGATTTGGTA 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TATCTCCAAACGATAAACGGAGTTTTAC 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAAAAAACATGATAAAAAGTTCATTTAAAGCTCAACCGTTTTTAGTAAGAAATACAATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TACTATCCTATTTTTATAAGTTATTTAGGGTTGCTAAATAGCTTATAAAAATAAAGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGTATTCACGTAAGCAAATAACCAAATCAAAGGATAGTATTTTGTTAGTTCAGACATGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGTATTCACGTAAGCAAATAACCAAATCAAAGGATAGTATTTTGTTAGTTCAGACATGGA 510
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                                                  Kuipers OP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                 94NL-0001935.
94NL-0001934.
                                                                                                                                                                                                                                95EP-0203153
                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= a
1278..1283
/*tag= b
1332..1446
/*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1252..1257
                                                                                                                                                                                                                                                                                                                                                                                  /product= Nisin A fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA;
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                                                                                                    INST
                                                                                                    ZUIVELOND
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Controlled lysis of transformed lactic acid bacteria to release intracellular proteins or RNA - by addn. of inducer to activate promoter to express antimicrobial peptide, useful for prodn. of
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Example 2; Fig 4b; 29pp; English

This sequence represents the nisin A promoter isolated from Lactococcus CC lactis. This sequence is used to control the DNA fragment of the method of the invention is for the controlled CC expression of a DNA fragment containing one or more genes of desired CC characteristics, in a lactic acid bacterium. The DNA fragment is under CC the control of a promoter for a microbial gene that encodes an expressed by the addition of a suitable inducer for transcription CC expressed by the addition of a suitable inducer for transcription CC expression of the DNA fragment causes the lysis of the microorganism CC used is an antimicrobial peptide produced by lactic acid bacterium. The cused, or alternatively results in the release of intracellular proteins CC (such as enzymes, membrane proteins, extracellular proteins and CC used, or alternatively results in the release of intracellular proteins CC antimicrobial peptides) or RNA. The method is particularly useful for CC producing dairy products containing a desired protein. The release of the intracellular enzymes provides accelerated maturing of fermented CC the intracellular enzymes provides accelerated maturing of fermented CC the intracellular enzymes provides accelerated maturing of inducer in a medium. Can be used to determine the concentration of a inducer in CC addition of the inducer.

Sequence 1446 BP; 488 A; 233 C; 244 G; 481 T; 0 other;

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Best Local :
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                                                                                                                                                                                                                                                                                                        1095
1395
                                                                                                                      1275
                            361
                                                                                       301
                                                                                                                                                                                                             181
                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                   1 AGTTGACGAATATTTAATAATTTTAATTAATATCTTGATTTTCTAGTTCCTGAATAATATA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                           h 53.5%;
Similarity 99.8%;
                                                                                                                                                                                                                                                                                                                         GAGATAGGTTTATTGAGTCTTAGACATACTTGAATGACCTAGTCTTATAACTATACTGAC 120
                                                                                                                                                                                                                                                                                                        GAGATAGGTTTATTGAGTCTTAGACATACTTGAATGACCTAGTCTTATAACTATACTGAC
                                                                                                                                                                                                                                                                                                                                                                  AGTTGACGAATATTTAATTAATTAATATCTTGATTTTCTAGTTCCTGAATAATATA
                                                                                                                                                                                                                                                                         AATAGAAACATTAACAAATCTAAAACAGTCTTAATTCTATCTTGAGAAAGTATTGGTAAT 180
CCACGCATTACAAGTATTTCGCTATGTACACCCCGTTGTAAAACAGGAGCTC
                 CCACGCATTACAAGTATTTCGCTATGTACACCCGGTTGTAAAACAGGAGCTC
                                                                               AGATACAATGATTTCGTTCGAAGGAACTACAAATAAATTATAAGGAGGCACTCAAAATG
                                                                                                                                      AGATACAATGATTTCGTTCGAAGGAACTACAAAATAAATTATAAAGGAGGACTCAAAATG
                                                                                                                                                                                 AATATTATTGTCGATAACGCGAGCATAATAAACGGCTCTGATTAAATTCTGAAGTTTGTT
                                                                                                                                                                                                             AATATTATTGTCGATAACGCGAGCATAATAAACGGCTCTGATTAAATTCTGAAGTTTGTT
                                                                                                                                                                                                                                           AATAGAAACATTAACAAATCTAAAACAGTCTTAATTCTATCTTGAGAAAGTATTGGTAAT 1214
                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 410.4; DB 17; Length 1446; Pred. No. 1.7e-73;
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 1446
                               412
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                                                             1394
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                                                                                                                                                                                  1274
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RESULT 6
ABK14453
ID ABK1
XX
AC ABK1
XX
AC ABK1
XX
AC ABK1
XX
DT 08-M
XX
            08-MAY-2002
                                 ABK14453;
                                                      ABK14453 standard; DNA; 1446
           (first entry)
                                                      ВР
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Lactococcus

lactis nisA

promoter sequence, from

Tn5276.

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The present invention relates to a new method for controlling expression CC of a gene. The method of the invention involves providing a DNA fragment CC comprising a gene under transcriptional control of a promoter, where the CC promoter is obtained from a Gram-positive gene for an antimicrobial copyride or a precursor of the peptide. The gene is found in a gene CC cluster for the synthesis of the antimicrobial peptide and the promoter is inducible by the peptide. The antimicrobial peptide of the invention CC is acceptable in food products. The method provides a homologous CC expression system in Lactococcus, which is able to give strict/absolute regulation of the gene expression using (in low concentrations) suitable inducers. High production of the desired protein, aminopeptidase N in capperiments, gave a specific activity of 25000 nmol/mg/min using 0.5 g/l clisin A as the inducer, a level that has never been reached before by use of other (constitutive) promoters. The present nucleic acid sequence corporates
                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Controlled expression of a gene for production of a protein comprises providing a DNA fragment under control of a promoter from an antimicrobial peptide, where the peptide induces the promoter
                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Fig 4b; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-107870/15.
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18-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -10_signal
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                                                                                                                                                                                                                                                                         411;
                                                                                                                                    61
                                                                                                                                                                                                                             н
                                                                                                                                                                                                                                                                                              Similarity
                                                                                                             GAGATAGGTTTATTGAGTCTTAGACATACTTGAATGACCTAGTCTTATAACTATACTGAC
                       AATAGAAACATTAACAAATCTAAAACAGTCTTAATTCTATCTTGAGAAAGTATTGGTAAT
                                                                                      GAGATAGGTTTATTGAGTCTTAGACATACTTGAATGACCTAGTCTTATAACTATACTGAC
                                                                                                                                                                              AGTTGACGAATATTTAATAATTTTAATAATATCTTGATTTTCTAGTTCCTGAATAATATA
                                                                                                                                                                                                          AGTTGACGAATATTTAATAATTTTAATATATCTTGATTTTCTAGTTCCTGAATAATATAT
                                                                                                                                                                                                                                                                                                                                                               1446
AATAGAAACATTAACAAATCTAAAACAGTCTTAATTCTATCTTGAGAAAGTATTGGTAAT
                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                             BP;
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94NL-0001935.
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/standard name= '
1317..1323
/*tan-
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1278..1283
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1252..1257
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0; Mismatches
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밁 δ 밁 Ś 밁 S

Total DNA was isolated from the L. lactis strains NIZO 22186 and NIZO R5. With the aid of the nisA gene of strain NIZO R5 as a p. a 4.5 kb HindIII fragment was identified in the total DNA strain NIZO 22186, which was then cloned in M13 mp18. The DNA sequence

sequence of

probe

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RESULT 7
AAQ30070
ID AAQ3
XX Lact
XX Lact
XX Lact
XX Lact
XX Cac
FT RBS
FT CDS
FT RBS
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strains which produce
                                                                                                                Example; Fig
                                                                                                                                                                                                                                                                                  WPI;
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02-APR-1993
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                                                                                                                                                                                   them,
                                                                                                                English.
                                                                                                                                                                                   related to nisin A - and Lactococcus them, useful as preservatives for foods
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              Flanagan AJ,
                                                                                                                                         26-AUG-1999.
                                                                                                                                                                                                                                                                                                           Nisin Z;
                                                                                                                                                                                                                                                                                                                                         Nisin Z gene of Lactobacillus lactis.
                                                                                                                                                                                                                                                                                                                                                                      09-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                          AAX87793 standard; DNA; 360 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 360 BP; 129 A; 52 C; 66 G;
                                                                                   18-FEB-1998;
                                                                                                             12-FEB-1999;
                                                                                                                                                                     WO9941978-A1
                                                                                                                                                                                                                                                                     Lactobacillus
                                          (PFIZ ) PFIZER INC. (PFIZ ) PFIZER LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                           {\bf Z}_i nis {\bf Z}_i lantibiotic; animal performance; growth conversion; bacteriocin; probiotic; ss.
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             Haxell
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             Rolph
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             express the performance enhancing polypeptide, is administered to the gastrointestinal tract, especially to an embryo or neonatal animal. If the polypeptide is nisin, it may also inhibit ruminal methane, decrease acetate to propionate ratios and prevent amino acid deamination. Administration of an appropriate bacterium which may act as a probiotic may also help control enteric pathogens in poultry. The polypeptide is produced continuously in the gut, maintaining a constant level. The protein is eventually degraded, leaving no residues in the meat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This is the nisin Z (nis Z) gene region of Lactobacillus lactis strain 22186. Nisin Z is a natural analogue of nisin A (see AAY06665), a lanthionine-containing bacteriocin. The invention relates to methods of enhancing performance in an animal by administering a bacterium capable of expressing a performance enhancing polypeptide such as nisin A or nisin Z. The enhanced performance results in improved growth rates and feed conversion efficiencies. The bacterium, which may be genetically modified to
                                       Bacteriocin; LL-2; gram positive bacteria; antimicrobial; food; PCR; polymerase chain reaction; amplification; inhibit; ss.
                                                                                 Bacteriocin
                                                                                                                                                     AAQ49150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel performance enhancing method resulting in improved growth rates and feed conversion efficiencies in animals
              Lactococcus lactis
                                                                                                             25-MAR-2003
10-MAR-1994
                                                                                                                                                                                AAQ49150 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 360 BP; 129 A; 52 C; 66 G; 113 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 71; 79pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCACCACGCATTACAAGTATTTCGCTATGTACACCCGGTTGTAAAACAGGAGCTCTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AATAATATTATTGTCGATAACGCGAGCATAATAAACGGCTCTGATTAAATTCTGAAGTTT
                                                                                                                                                                                                                                                                     CAAAGGATAGTATTTTGTTAGTTCAGACATGGATACTATCCTATTTTTATAAGTTATTTA 537
                                                                                                                                                                                                                                                                                                             GGTTGTAACATGAAAACAGCAACTTGTAATTGTAGTATTCACGTAAGCAAATAACCAAAT
                                                                                                                                                                                                                                                                                                                              GGTTGTAACATGAAAAACAGCAACTTGTCATTGTAGTATTCACGTAAGCAAATAACCAAAT 477
                                                                                                                                                                                                                                                                                                                                                                                                                          AATAATATTATTGTCGATAACGCGAGCATAATAAACGGCTCTGATTAAATTCTGAAGTTT
                                                                                                                                                                                                                                                                                                                                                                    TCACCACGCATTACAAGTATTTCGCTATGTACACCCGGTTGTAAAACAGGAGCTCTGATG
                                                                                 gene.
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(first en
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99.7%;
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Pred. No. 4.3e-63;
0; Mismatches 1
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RESULT 10
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Best Local Similarity
Matches 320; Conserv
                                                                                                                                                                                                                                                                                                                                                                                The sequence (AAQ49150) was amplified using primers (AAQ49151-52). encoded protein inhibits selected gram positive bacteria and this property is enhanced if further purified by HPLC. The materials being treated to provide inhibition are preferably foods, although other materials can be treated.
        25-MAR-2003
12-MAY-1993
                                   AAQ34782;
                                                   AAQ34782 standard;
                                                                                                                                                                                                                                                                                                                                                Sequence 321 BP; 114 A; 51 C; 63 G; 93 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteriocin from Lactococcus lactis subspecies lactis inhibitory against Gram-positive bacteria
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14-MAY-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 13-14 (col 15,16,17,18); 14pp;
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                                                                                                                                                                                                                                                                                       CGCGAGCATAATAAACGGCTCTGATTAAATTCTGAAGTTTTGTTAGATACAATGATTTCGT
                                                                                                         GTTCAGACATGGATACTATCC 518
                                                                                                                                                                                                                CTTGGATTTGGTATCTGTTTCGAAGAAAGATTCAGGTGCATCACCACGCATTACAAGTAT
                                                                                                                                                                                                                                                   TCGAAGGAACTACAAAATAAATTATAAGGAGGCACTCAAAATGAGTACAAAAGATTTTAA
                                                                                              GTTCAGACATGGATACTATCC
                                                                                                                                            AACTTGTCATTGTAGTATTCACGTAAGCAAATAACCAAATCAAAGGATAGTATTTTGTTA
                                                                                                                                                                                                                                         TCGAAGGAACTACAAAATAAATTATAAGGAGGCACTCAAAATGAGTACAAAAGATTTTAA
                                                                                                                                                                                                                                                                            CGCGAGCATAATAAACGGCTCTGATTAAATTCTGAAGTTTGTTAGATACAATGATTTCGT
                                                                                                                                 AACTTGTAATTGTAGTATTCACGTAAGCAAATAACCAAATCAAAGGATAGTATTTTGTTA
                                                                                                                                                                    TTCGCTATGTACACCCGGTTGTAAAACAGGAGCTCTGATGGGTTGTAACATGAAAACAGC
                                                                                                                                                                              TTCGCTATGTACACCCGGTTGTAAAACAGGAGCTCTGATGGGTTGTAACATGAAAAACAGC
                                                                                                                                                                                                       CTTGGATTTGGTATCTGTTTCGAAGAAAGATTCAGGTGCATCACCACGCATTACAAGTAT
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ilarity 99.7%;
Conservative
        (updated)
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92US-0882079.
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/product= Bacteriocin
                                                   DNA;
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                                                                                                                                                                                                                                                                                                             Score 319.4; DB 1
Pred. No. 2.9e-55;
0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                              DB 14; Length 321;
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Best Local :
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The sequence is that of the bacteriocin LL-2 precursor gene, the precursor can be used in a method for the inhibition of Gram-positive bacteria. LL-2 is especially useful for treatment of food, although other non-food materials may also be treated.

(Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 321 BP; 114 A; 51 C; 63 G; 93 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 13; 14pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteriocin LL-2 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inhibition of Gram-positive bacteria - using bacteriocin from Lactococcus lactis sub-species lactis NRRL B-18809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lactococcus lactis sub-species lactis
                                 GTTCAGACATGGATACTATCC 518
                                                                                                            AACTIGTCATIGTAGTATTCACGTAAGCAAATAACCAAATCAAAGGATAGTATTTTGTTA
                                                                                                                                                                                            TTCGCTATGTACACCCGGTTGTAAAACAGGAGCTCTGATGGGGTTGTAACATGAAAACAGC
                                                                                                                                                                                                                                                                                    CTTGGATTTGGTATCTGTTTCGAAGAAAGATTCAGGTGCATCACCACGCATTACAAGTAT
                                                                                                                                                                                                                                                                                                                                                                          TCGAAGGAACTACAAAATAAATTATAAGGAGGCACTCAAAATGAGTACAAAAGATTTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                       CGCGAGCATAATAAACGGCTCTGATTAAATTCTGAAGTTTGTTAGATACAATGATTTCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGCGAGCATAATAAACGGCTCTGATTAAATTCTGAAGTTTGTTAGATACAATGATTTCGT
                                                                                                                                                                                                                                                             CTTGGATTTGGTATCTGTTTCGAAGAAAGATTCAGGTGCATCACCACGCATTACAAGTAT
                                                                                                                                                                                                                                                                                                                                                 TCGAAGGAACTACAAAATAAATTATAAGGAGGCACTCAAAATGAGTACAAAAGATTTTAA
                                                                                                                                                                     TTCGCTATGTACACCCGGTTGTAAAACAGGAGCTCTGATGGGTTGTAACATGAAAAACAGC
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101..169
/*tag= b
170..271
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99.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 319.4; DB 14, -- Pred. No. 2.9e-55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 321;
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                                                                                                                                                                                                                               Best Local Similarity Matches 320; Conserv
                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                            The isolated bactriccin obtained from the polypeptide precursor has an inhibitory activity against selected Gram positive bacteria. The amount of bacteriocin required to provide inhibition is 15-100 arbitrary units per gram of material. The materials being treated with the bactericcin to provide inhibition are especially foodstuff
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated and purified polypeptide from Lactococcus lactis sub species lactis - has inhibitory activity against gram-positive bacteria for e.g. food etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Column 17-18; 13pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Henderson JT,
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14-MAY-1992;
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21-JAN-1994
                                                                                                                                                                                                                                                                                      Sequence 321 BP; 114 A; 51 C; 63 G; 93 T; 0 other;
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                                                                                                                                                                                                                                                                                                              with the bacteriocin to provide inhibition are especially (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lactococcus lactis (subspecies lactis)
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DB; AAR39312.
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                                                                                                                                                                                        CGCGAGCATAATAAACGGCTCTGATTAAATTCTGAAGTTTTGTTAGATACAATGATTTCGT
                    TTCGCTATGTACACCCGGTTGTAAAACAGGAGCTCTGATGGGTTGTAACATGAAAACAGC
                                                                                                                                           TCGAAGGAACTACAAAATTAATAAGGAGGCACTCAAAATGAGTACAAAAGATTTTAA 317
TTCGCTATGTACACCCGGTTGTAAAACAGGAGCTCTGATGGGTTGTAACATGAAAACAGC
                                                        CTTGGATTTGGTATCTGTTTCGAAGAAAGATTCAGGTGCATCACCACGCATTACAAGTAT
                                                                                   CTTGGATTTGGTATCTGTTTCGAAGAAAGATTCAGGTGCATCACCACGCATTACAAGTAT
                                                                                                                TCGAAGGAACTACAAAATTAAAGGAGGCACTCAAAATGAGTACAAAAGATTTTAA
                                                                                                                                                                       CGCGAGCATAATAAACGGCTCTGATTAAATTCTGAAGTTTGTTAGATACAATGATTTCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bacteriocin coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inhibition; polypeptide; Lactococcus lactis;
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92US-0882715.
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/product= Bacteriocin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vanwassenaar PD,
                                                                                                                                                                                                                            Score 319.4; DB 14; Length Pred. No. 2.9e-55; 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                        Length 321;
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This invention describes a novel plasmid (I), designated pCD6 for transformation of Clostridium difficile. The invention describes a method CC l) for (a) expressing a heterologous gene sequence in C. difficile which CC comprises providing a plasmid containing the heterologous gene sequence, comprises providing a plasmid containing the heterologous gene sequence, comprises contains a gene coding for a selectable marker, selecting CC for C. difficile that express the selectable marker, (2) for making a comprises; (3) for identifying a C. difficile in the presence of a regulating factor that promotes expression of C. difficile virulence factor which comprises culturing C. difficile in the absence of, and in the presence of a regulating factor that promotes expression of C. difficile virulence factors and identifying a putative virulence factor whose expression is comprises (a) transforming a gram positive bacterial genome which comprises; (a) transforming a gram positive bacteria with a plasmid, where the plasmid comprises an inducible promoter and replication of the transforming a gram positive bacteria with a plasmid the comprises and selecting for a selectable marker, and the transforming a gram positive bacteria with a plasmid the comprises an suppressible promoter and replication of the plasmid comprises an suppressible promoter and replication of the plasmid comprises an suppressible promoter and replication of the plasmid comprises an suppressible promoter and replication of the plasmid comprises an suppressible promoter and replication of the plasmid comprises an suppressible promoter and replication of the plasmid comprises an suppressible promoter and replication of the plasmid comprises and suppressible promoter and replication of the plasmid comprises an suppressible promoter and replication of the plasmid comprises and suppressible promoter and replication of the plasmid comprises and suppressible promoter and replication of the plasmid comprises and suppressible promoter and replication of the plasmi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAI69229 standard; DNA; 212 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MICR-) MICROBIOLOGICAL RES AUTHORITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -10_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -35_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           plasmid, designated pCD6, useful for transformation of Clostridium
ficile and for expressing gene in Clostridium difficile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2002-010908/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Fig 12; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PMTL910E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTTCAGACATGGATACTATCC 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTTCAGACATGGATACTATCC 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AACTTGTAATTGTAGTATTCACGTAAGCAAATAACCAAATCAAAGGATAGTATTTTGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AACTTGTCATTGTAGTATTCACGTAAGCAAATAACCAAATCAAAGGATAGTATTTTGTTA 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and for expressing gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= a
94..100
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers 71..77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Elmore MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O'Keeffe KMT
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RESULT 13
AAQ50289
ID AAQ50
XX AAQ50
XX AAQ50
XX DT 25-MA
DT 25-MA
DT 03-MA
XX Itacto
XX Niein
KW Niein
KW lanti
XX WO932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 206; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transformation takes place in the absence of the suppressor, adding the suppressor, and selecting for bacteria expressing the selectable marker; (5) for identifying a C. difficile methylase gene which comprises identifying the sequence of a bacterial methylase gene, comparing the sequence of the gene with the genome of a strain of C. difficile, identifying a region of the genome that contains at least 30% homology with the bacterial methylase gene, and expressing that region; (I) is useful for expressing a gene in C. difficile by making (I) containing that gene and transforming C. difficile with (I). (I) is useful for containing transforming C. difficile with (I). (I) is useful for containing transforming C. difficile with (I) for identification of a vector that integrates into Clostridia. This sequence a DNA fragment from the plasmid pMTL910E which is used to illustrate the method of the
                                                        antimicrobial use in food industry
                                                                                     New organisms able to express genes for nisin maturation, native pre-nisin - useful for producing variant nisin(s)
                                                                                                                                                                                                                           Dodd HM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eschericia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nisin; antibiotic; food; spoilage; pathogens; industrial processes; lantibiotic; Lactococcus lactis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAR-2003 (updated)
03-MAY-1994 (first en
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ50289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 212
                                                                                                                                                                       WPI; 1993-336920/42.
                                                                                                                                                                                                                                                                                                                                       02-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-OCT-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9320213-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lactose operon promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ50289 standard; DNA; 546 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plasmid includes a sequence coding for a selectable marker, and the
                                                                                                                                                                                                                                                                                 (AGRI-) AGRIC & FOOD RES COUNCIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92 GAATGACCTAGTCTTATAACTATACTGACAATAGAAACATTAACAAATCTAAAAACAGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAATTCTATCTTGAGAAAGTATTGGTAATAATATTATTGTCGATAACGCGAGCATAATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANATAAATTATAAGGAGGCACTCAAAATGAGT 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCATGACCTAGTCTTATAACTATACTGACAATAGAAACATTAACAAATCTAAAAACAGTCT
                                                                                                                                                                                                                           Gasson MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAATAAATTATAAGGAGGCACTCGACAATATT 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAATTCTATCTTGAGAAAGTATTGGTAATAATATTATTGTCGATAACGCGAGCATAATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP; 83 A; 31 C;
                                                                                                                                                                                                                                                                                                                                       92GB-0007267.
                                                                                                                                                                                                                                                                                                                                                                                             93WO-GB00676.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 202.4; DB 24;
Pred. No. 8.9e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33 G; 65 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                              but not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from
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Disclosure; Figure 5; 62pp; English

activity compared to nisin

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Sin
Matches 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nisin is a highly modified peptide antibiotic produced by certain bacteria e.g. strains of Lactococcus lactis. It has efficient antimicrobial activity against a wide range of Gram positive bacteria which are food pathogens or spoilage organisms. The genes involved in nisin maturation can be used to transform other microbes which are unable to secrete the natural nish nisin. These organisms can however modify nisin and translocate it out of the cell. This provides an effective means of producing variant nisins which are useful as antimicrobial agents in conditions of high pH where natural nisin is ring-opened and loses its antimicrobial properties. Variant nish genes were placed under the regulation of the lactose operon promoter ansd used to transform cells.
                                  WPI; 1997-225847/20.
P-PSDB; AAY31659.
                                                                                                                    28-SEP-1995;
                                                                                                                                            30-SEP-1996;
                                                                                                                                                                   03-APR-1997
                                                                                                                                                                                           WO9711713-A1
                                                                                                                                                                                                                                        mat_peptide
                                                                                                                                                                                                                                                                        sig_peptide
                                                                                                                                                                                                                                                                                                                                     Chimeric -
Chimeric -
                                                                                                                                                                                                                                                                                                                                                                        preservative;
                                                                                                                                                                                                                                                                                                                                                                                    Nisin; subtilin; lantibiotic; chimera; mutant; bacteriocide;
                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding subtilin-nisin chimera.
                                                                                                                                                                                                                                                                                                                                                                                                                                  09-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX87829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX87829 standard; DNA; 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 546 BP; 229 A; 62 C; 78 G; 177 T; 0 other;
           Lantibiotic mutants and chimera(s) -
                                                                                             (UYMA-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h 11.1%;
Similarity 97.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AATAAATTATAAGGAGGCACTCAAAATG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AATAAATTATAAGGAGGCACTCAAAATG
                                                                                                                                                                                                                                                                                                                                     Lactococcus lactis. Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                             MARYLAND BALTIMORE
                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                    95US-0535494.
                                                                                                                                            96WO-US15160
                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                      /*tag=
                                                                                                                                                                                                                   'note= "Sub(1-11)-Nis(12-32)'
                                                                                                                                                                                                                                                    'note= "subtilin signal peptide'
                                                                                                                                                                                                                                റ
                                                                                                                                                                                                                                                                  σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 84.8; DB 14;
Pred. No. 4.1e-08;
           having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; LZ
. 4.1e-08;
. 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          546
            enhanced
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
            stability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               546;
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This polynucleic acid (I) encodes Example; Fig 2; 60pp; English.

a chimeric pre-peptide (see

あいつかして

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RESULT 15
ABQ701.86
ID ABQ70
XX ABQ70
XX ABQ70
XX ARTib
XX ARTib
KW Infec
XX ARTib
KW INFec
XX 11-AP
XX 11-AP
XX 04-OC
XX (INSP
PA (CNRS
XX (INSP
PA (CNRS
XX WPI;
XX New g
PT treat
XX New g
PT treat
XX New g
PT treat
XX Claim
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               provides lantibiotic mutants and chimeras (see also AAY31658) ha enhanced activity and stability compared to nisin and subtilin. They can be produced by cultivation of transformed host cells an used e.g. as food preservatives to treat, kill or inhibit the growth of microorganisms and/or their spores.
                                                                                                                                                                        (INSP )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY31659) composed of a subtilin leader region and a subtilin-nisin fusion comprising residues 1-11 of Bacillus subtilis subtilin and residues 12-32 of Lactococcus lactis nisin. The chimera was not efficiently processed by B. subtilis into a functional lantibiotic. A heterogeneous mixture of products was produced, none of the products having the expected properties of a correctly processed polypeptide. However, the mixture contained a minor component with a specific activity that expected that of nicin
                 Claim
                                             New genomic sequences from Listeria species, useful treatment and prevention of infection, also related antibodies and modulators -
                                                                                                                                                                                                                     04-OCT-2000; 2000FR-0012697
                                                                                                                                                                                                                                                    04-OCT-2001; 2001WO-FR03061
                                                                                                                                                                                                                                                                                                                WO200228891-A2
                                                                                                                                                                                                                                                                                                                                             Listeria monocytogenes 4b
                                                                                                                                                                                                                                                                                                                                                                            Antibacterial; Listeria; food contamination; mutational analysis; infection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                         Listeria monocytogenes 4b contig DNA sequence #128.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABQ70186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABQ70186 standard; DNA; 878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 144 BP; 49 A; 32 C; 32 G; 31 T; 0 other;
                                                                                                          WPI; 2002-332479/37.
                                                                                                                                         Kunst F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         346
            14; SEQ ID 2999; 180pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INST PASTEUR.
CNRS CENT NAT RECH SCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGAGCTCTGATGGGTTGTAACATGAAAAACAGCAACTTGTCATTGTAGTATTCACGTAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GATTCAGGTGCATCACGCATTACAAGTATTTCGCTATGTACACCCGGTTGTAAAACA 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GATTCGAAAATCACTCCGCAATGGAAAAGTGAATCACCTTGTACACCCGGGTGTAAAAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAATAGGTAACCAAATAGGTA 141
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Pred. No. 1.4e-07
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                                                          for detection, polypeptides,
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                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to nucleic acid sequences (ABQ67188-ABQ71212) from Listeria sp. The sequences are useful as probes and primers for identification and/or detection of Listeria (e.g. as contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be used to screen for compounds that modulate gene expression, replication and pathogenicity of Listeria (potential therapeutic agents), also for
                                                                                                                                                                                                                                                                                                                                                                                               anti-Listeria vaccines.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic for the printed specification, but was obtained pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                      Sequence 878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  treating infections by Listeria,
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883
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                                                                                                        123 TAGAAACATTAACAAATCTAAAACAGTCTTAATTCTATCTTGAGAAAGTATTGGTAATAA
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TAGT 691
                              TATT 186
                                                                     TCGAAACTCCAGCATATAATAGCAAAGATGCATGGGTATGTCATAAACTATGAATCGTAA
                                                                                                                                             GATATGTTTCCTGGGTAGTAGTCATACTTGAATGACCTAACCTATTCGCAACACTAGCAA
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                                                                                                                                                                                                                                                       TTGACGAATATTTAATAATTTTATTAATATCTTGATTTCTAGTTCCTGAATAATATAGA
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                                                                                                                                                                                                                                                                                                               10.4%;
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                                                                                                                                                                                                                                                                                                               Score 80; DB 24;
Pred. No. 3.9e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and are useful
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                                                                                                                                                                                                                                                                                                                                 Length 878;
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Search completed: January 12, Job time : 280 secs 2004, 11:30:05

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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Perfect score:
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

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US-07-882-775-1
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US-08-836-687B-27
US-08-836-687B-27
US-08-773-731A-3
US-08-535-494-8
US-08-220-033-6
US-08-773-731A-7
US-08-986-617-6
US-08-986-617-6
US-08-986-617-8
US-08-220-033-8
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TYPE: DNA
ORGANISM: Lactococcus
US-08-836-687B-29
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US-08-836-687B-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Gasson, Michael John
APPLICANT: Dodd, Helen Mair
TITLE OF INVENTION: PRODUCTION OF VARIANT NISIN
FILE REFERENCE: 20747/70
CURRENT APPLICATION NUMBER: US/08/836,687B
CURRENT FILING DATE: 1995-11-20
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 29
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Best Local
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Similarity 100.0%; Pred. No. 2.2e-140;
75; Conservative 0; Mismatches 0;
                   TATTCACGTAAGCAAATAACCAAATCAAAGGATAGTATTTTGTTAGTTCAGACATGGATA
                                                                                                                                                                                         AATAAATTATAAGGAGGACTCAAAATGAGTACAAAAGATTTTAACTTGGATTTGGTATC
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US-08-986-617-1
US-08-773-731A-21
US-08-77981-525-3
US-08-220-033-3
US-08-465-491-3
US-08-232-463-14
US-08-232-463-14
US-08-232-463-14
US-08-920-812-6
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 448 base pairs
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                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
SOFTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/773,731A
FILING DATE: 24-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/313,123
FILING DATE: 18-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00676
FILING DATE: 01-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9207267.7
FILING DATE: 02-APR-1992
PRIOR DATE: US-DAWATION
APPLICATION DATA:
APPLICATION NUMBER: GB 9207267.7
                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: Brady, Jr., James W.
REGISTRATION NUMBER: 32,115
REFERENCE/DOCKET NUMBER: E828
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-785-9700
TELEPAX: 202-887-0689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: DICKSTEIN, SHAPIRO, MORIN & OSHINSKY LLP
STREET: 2101 L Street N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gasson, Michael J. APPLICANT: Dodd, Helen M. TITLE OF INVENTION: NISINS NUMBER OF SEQUENCES: 21
                  FEATURE:
NAME/KEY:
                                                     MOLECULE TYPE:
                                                                                 STRANDEDNESS:
                                                                                                  TYPE: nucleic acid
                                                                          TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Washington
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                                                                                     GAAAAAACATGATAAAAAGTTCATTTAAAGCTCAACCGTTTTTAGTAAGAAATACAATTT
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                                                                                                                TACTATCCTATTTTTATAAGTTATTTAGGGTTGCTAAATAGCTTATAAAAATAAAGAGAG
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98.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 440; DB 3;
Pred. No. 9.8e-89;
0; Mismatches 8
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RESULT 3 US-08-560-007B-4 Sequence 4, Application US/08560007B
Patent No. 5914248
GENERAL INFORMATION:
APPLICANT: KUIPERS, OSCAR PAUL
APPLICANT: DE VOS, WILLEM MEINDERT
TITLE OF INVENTION: METHOD FOR CONTROLLING THE GENE
TITLE OF INVENTION: EXPRESSION IN LACTIC ACID BACTERIA CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS: OPERALLING
OPERAPELIES
SOFTWARE: WORDERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/560,007B COMPUTER READABLE FORM: MEDIUM TYPE: FLOPPY DISK CORRESPONDENCE ADDRESS:
ADDRESSEE: THE WEBB LAW FIRM
STREET: 700 KOPPERS BUILDING, NUMBER OF SEQUENCES: APPLICATION NUMBER: US/01 FILING DATE: 17 NOV 1995 CITY: PITTSBURGH STATE: PENNSYLVANIA COUNTRY: UNITED STATES OF COMPUTER: NEC 286
OPERATING SYSTEM: STRANDEDNESS: TOPOLOGY: LENGTH: 15219-1818 NUCLEIC ACID UNKNOWN 286 SINGLE DOS 4. AMERICA 436 SEVENTH AVENUE

US-08-560-007B-4

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US-08-129-151A-1
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
SOFTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/129,151A
FILING DATE: 07-CCT-1993
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION UMMBER: NL 9100634
FILING DATE: 11-APR-1991
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMMBER: PCT/NL92/00068
FILING DATE: 09-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, ANDERS: 32,925
REGISTRATION NUMBER: 32,925
REFERENCE/DOCKET NUMBER: B0 37078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: SIEZEN, ROCLART J.

APPLICANT: KUIPERS, OBCAR P.

TITLE OF INVENTION: LANTIBIOTICS SIMILAR TO NISIN A, LACTIC
TITLE OF INVENTION: ACID BACTERIA WHICH PRODUCE SUCH LANTIBIOTICS,
TITLE OF INVENTION: CONSTRUCTING SUCH LACTIC ACID BACTERIA AND METH
TITLE OF INVENTION: PRESERVING FOODSTUFFS WITH ETC.
                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: DE VOS, Willem M. APPLICANT: SIEZEN, Roelant JAPPLICANT: KUIPERS, OSCAR P.
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                                                                                                                                                                                                                                                                                                                                             COUNTRY: U
ZIP: 22202
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                                                                                                                                                                                                                                                                                                                                                                                               CITY: Arlington
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Patent No. 592894
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/715,579
FILING DATE: 19-SEP-1996
CLASSIFICATION: 435
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TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION:
TITLE OF INVENTION:
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NAME/KEY:
LOCATION:
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APPLICANT: SIEZEN, I
APPLICANT: KUIPERS,
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                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                  CITY: Arlington
                                                                                                                                           ZIP:
                                                                                                                                                                        STATE:
                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single TOPOLOGY: linear
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                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                      ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                          Application US/08715579
                                                                                                                                                        USA
                                                                                                                                                                                                    3: c/o YOUNG & THOMPSON 745 South 23rd Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 703/521-2297
703/685-0573
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), Oscar P.
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99.7%;
                                                                                                                                                                                                                                                                LANTIBIOTICS SIMILAR TO NISIN A, LACTIC
ACID BACTERIA WHICH PRODUCE SUCH LANTIBIOTICS, METHOD CONSTRUCTING SUCH LACTIC ACID BACTERIA AND METHOD FOR PRESERVING FOODSTUFFS WITH ETC.
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Pred. No. 9.5e-71;
0; Mismatches 1
                                                                                                                                                                                                       Second Floor
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                                                               #1.25
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FOR

PRIOR APPLICATION DATA:
APPLICATION NUMBER:

US 08/129,151

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RESULT 6
US-07-721-774A-1
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; LOCATION:
US-08-715-579-1
                                                                                                                                                                Sequence 1, Application US/07721774A Patent No. 5173297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 46.7%;
Best Local Similarity 99.7%;
Matches 359; Conservative
     GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Vedamuthu, Ebenezer R; Henderson, James T;
APPLICANT: Vedamuthu, Ebenezer R; Henderson, James T;
APPLICANT: Marugg, John D; van Wassenaar, Pieter D
TITLE OF INVENTION: No. 5173297el Bacteriocin From Lactococcus lactis
TITLE OF INVENTION: Subspecies lactis
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 703/685-0573
TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO: 1:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: NL 9100634
FILING DATE: 11-APR-1991
PRIOR APPLICATION UNMBER: PCT/NL92/000
APPLICATION UNMBER: PCT/NL92/000
FILING DATE: 09-APR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: PATCH, Andrew J.
REGISTRATION NUMBER: 32,925
REFERENCE/DOCKET NUMBER: BO 37078
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703/521-2297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
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Pred. No. 9.5e-71;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 360;
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US-07-882-715-1 ; Sequence 1, Application US/07882715 ; Patent No. 5231165

RESULT 7

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TELEX: NO. 5173297e
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 321 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 41.6%;
Best Local Similarity 99.7%;
                                                                                                                                                                                                                                                                                                                                                                                            Matches
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NAME: Ian C. McLeod
REGISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: MT 4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 347-4100
TELEPAX: (517) 347-4103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: OF
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SOFTWARE: ASCII text editor
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
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STRAIN: NRRL-B-18809
INDIVIDUAL ISOLATE: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 199107 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CELL TYPE: unicellular organism
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301
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                GTTCAGACATGGATACTATCC 518
                                                                AACTTGTAATTGTAGTATTCACGTAAGCAAATAACCAAATCAAAGGATAGTATTTTGTTA
                                                                                  AACTTGTCATTGTAGTATTCACGTAAGCAAATAACCAAATCAAAGGATAGTATTTTGTTA
                                                                                                                                TTCGCTATGTACACCCGGTTGTAAAACAGGAGCTCTGATGGGTTGTAACATGAAAACAGC
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GTTCAGACATGGATACTATCC
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101 to 271
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Pred. No. 3.8e-62;
0; Mismatches 1;
321
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 321 bass
                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                            Query Match 41.6%;
Best Local Similarity 99.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Ian C. McLeod
REGISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: MT 4.1-142
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 347-4100
TELEFAX: (517) 347-410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/721,774
FILING DATE: July 1, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN: NRRL-B-18809
INDIVIDUAL ISOLATE: LLA-2.0
CELL TYPE: Unicellular organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
FILING DATE: 199205
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: Acer
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: bacteriocin encoding DNA LOCATION: 101 to 271
                                                                                                                                                                                                                                                                                                                                                IDENTIFICATION METHOD: sequencing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: NUCLEIC ACID
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                       378
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                                                                                                                                                                                                              198 CGCGAGCATAATAAACGGCTCTGATTAAATTCTGAAGTTTGTTAGATACAATGATTTCGT
                                                                                                                                                                                                                                                            320;
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TTCGCTATGTACACCCGGTTGTAAAACAGGAGCTCTGATGGGTTGTAACATGAAAACAGC
                                                                                CTTGGATTTGGTATCTGTTTCGAAGAAAGATTCAGGTGCATCACCACGCATTACAAGTAT 377
                                                                                                                                                       TCGAAGGAACTACAAAATAAATTATAAGGAGGCACTCAAAATGAGTACAAAAGATTTTAA 317
                                                                                                                       TCGAAGGAACTACAAAATAAATTATAAGGAGGCACTCAAAATGAGTACAAAAGATTTTAA
                                                                                                                                                                                        CGCGAGCATAATAAACGGCTCTGATTAAATTCTGAAGTTTGTTAGATACAATGATTTCGT
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                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ian C. McLeod
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Diskette, 5.25 inch, 360 Kb storage
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Lactococcus lactis subspecies
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                                                                                                                                                                                                                                                            0,
                                                                                                                                                                                                                                                                            Score 319.4; DB 1 Pred. No. 3.8e-62;
                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                            DB 1; Length 321;
                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                            0
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Query Match 41.9
Best Local Similarity 99.7
Matches 320; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (517) 347-410
TELEX: NO. 5232849e
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/721,
FILING DATE: July 1, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Ian C. WcLeod
REGISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: MT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 2. STREET: 4. STREET: Michigan 115A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF
                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 347-4100
TELEPAX: (517) 347-4103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOPTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/
FILING DATE: 19920514
CLASSIFICATION: 435
                                                                                                                 FEATURE:
NAME/KEY:
                                                                                                                                                                                                                  ORIGINAL SOURCE:
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OPERATING SYSTEM: MS-DOS
                                                                                 LOCATION: 101 to 271 IDENTIFICATION METHOD:
                                                                                                                                                    CELL TYPE:
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                                                                                                                                                                                                                                                                                                                   TYPE: NUCLEIC ACID
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JAL ISOLATE:
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101 to 271
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99.7%;
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                                                                                  sequencing
Score 319.4; DB 1;
Pred. No. 3.8e-62;
0; Mismatches 1;
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                                Length 321;
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Sequence 19. Application US/08836687B

PATENT NO. 6448034

GENERAL INFORMATION:
APPLICANT: Gasson, Michael John
APPLICANT: Dodd, Helen Mair
TITLE OF INVENTION: PRODUCTION OF VARIANT NISIN
FILE REFERENCE: 20747/70

CURRENT APPLICATION NUMBER: US/08/836,687B

CURRENT FILING DATE: 1995-11-20

NUMBER OF SEQ ID NOS: 51

SOFTWARE: PATENTIN Ver. 2.1

SEQ ID NO 19
LENGTH: 300

TYPE: DNA
; Sequence 22, Application US/08836687B
              RESULT 10
US-08-836-687B-22
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Lactococcus sp.
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100.0%; Prr
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APPLICANT: Gasson, Michael John
APPLICANT: Dodd, Helen Mair
TITLE OF INVENTION: PRODUCTION OF VARIANT NISIN
FILE REFERENCE: 20747/70
CURRENT APPLICATION NUMBER: US/08/836,687B
CURRENT FILING DATE: 1995-11-20
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 22
LENGTH: 300
TYPE: DNA
ORGANISM: Lactococcus sp.
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APPLICANT: Dodd, Helen Maix
TITLE OF INVENTION: PRODUCTION OF VARIANT NISIN
FILE REFERENCE: 20747/70
CURRENT APPLICATION NUMBER: US/08/836,687B
CURRENT FILING DATE: 1995-11-20
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 21, Application US/08836687B Patent No. 6448034 GENERAL INFORMATION:
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GENERAL INFORMATION:
                                                                                                                                                      Matches
                                                                                                                                                                                 Query Match
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Best Local Similarity
                                                                                                                                                                                                                              LENGTH: 300
TYPE: DNA
ORGANISM: Lactococcus
                                                                                                                                                                   Match 38.3%;
Local Similarity 98.7%;
327 GGTATCTGTTTCGAAGAAAGATTCAGGTGCATCACCACGCATTACAAGTATTTCGCTATG
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                                                                                                                                                   Score 293.6; DB 4; Length 300; Pred. No. 1.8e-56; O; Mismatches 4; Indels 0
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Pred. No. 3.6e-57;
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US-08-836-687B-23

; Sequence 23, Application US/08836687B
; Sequence 23, Application US/08836687B
; Patent No. 6448034
; GENERAL INFORMATION:
   APPLICANT: Gasson, Michael John
   APPLICANT: Dodd, Helen Mair
; TITLE OF INVENTION: PRODUCTION OF VARIANT NISIN
; FILE REFERENCE: 20747/70
; CURRENT APPLICATION NUMBER: US/08/836,687B
; CURRENT FILING DATE: 1995-11-20
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: Patentin Ver. 2.1
; SOTTWARE: Patentin Ver. 2.1
; SEQ ID NO 23
; LENGTH: 300
                                              RESULT 13

US-08-836-687B-25

; Sequence 25, Application US/08836687B

; patent No. 6448034
; patent No. 6448034
; patent INFORMATION:
APPLICANT: Dodd, Helen Mair
i TITLE OF INVENTION: PRODUCTION OF VARIANT NISIN
FILE REFERENCE: 20747/70
; CURRENT APPLICATION NUMBER: US/08/836,687B
; CURRENT FILING DATE: 1995-11-20
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 25
; LENGTH: 710
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; ORGANISM: Lactococcus
US-08-836-687B-23
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Best Local Similarity
Matches 296; Conserv
TYPE: DNA
ORGANISM: Lactococcus sp.
                                   ENGTH: 300
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ilarity 98.7%;
Conservative
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Pred. No. 1.8e-56;
0; Mismatches 4
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APPLICANT: Gasson, Michael John
APPLICANT: Dodd, Helen Mair
ITTLE OF INVENTION: PRODUCTION OF VARIANT NISIN
FILE REFERENCE: 20747/70
CURRENT APPLICATION NUMBER: US/08/836,687B
CURRENT FILING DATE: 1995-11-20
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: DAA
CORGANISM: Lactococcus sp.
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                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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Pred. No. 1.8e-56;
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RESULT 15 US-08-773-731A-3

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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Flomper of the compatible
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/73,731A
FILING DATE: 24-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/313,123
FILING DATE: 18-NOV-1994
PRIOR APPLICATION NUMBER: PCT/GB93/00676
FILING DATE: 01-APR-1993
PRIOR APPLICATION NUMBER: PCT/GB93/00676
FILING DATE: 01-APR-1993
PRIOR APPLICATION NUMBER: B9207267.7
FILING DATE: 02-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Brady, Jr., James W.
REGISTRATION NUMBER: 32,115
REFERENCE/DOCKET NUMBER: B280.016/P016
FILEPHONE: 202-887-0689
INFORMATION: 202-887-0689
INFORMATION: CHARACTERISTICS:
Search completed: January 12, 2004, 12:06:14 Job time: 69 secs
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                                                                                                                                                                                                                                                                  Query Match 11.1%; Score 84.8; DB 3; Length 546; Best Local Similarity 97.7%; Pred. No. 2.4e-10; Matches 86; Conservative 0; Mismatches 2; Indels
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APPLICANT: Gasson, Michael J.
APPLICANT: Dodd, Helen M.
TITLE OF INVENTION: NISINS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 546 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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ZIP: 20037
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CITY: Washington
STATE: DC
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Maximum Match 100%
Listing first 45 summaries
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48.4
48.2
48.2
49.2
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seq length: 2000000000
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767
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    6.4 6361
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6.3 4985
6.3 17594
6.2 7351
6.1 5452
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6.1 17294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
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/cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
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                  3 US-10-082-618-8

3 US-10-311-455-1721

10 US-10-312-841-1

3 US-10-311-455-1113

3 US-10-311-455-1100

3 US-10-240-485-1100

3 US-10-094-240-10

5 US-10-094-240-10

9 US-10-311-455-199

9 US-10-311-455-199

1 US-10-311-455-122

1 US-10-311-851-84

1 US-10-311-85-859

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1 US-10-311-85-859
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Sequence 8, Appli
Sequence 1721, Ap
Sequence 1, Appli
Sequence 113, Ap
Sequence 1100, Ap
Sequence 1100, Ap
Sequence 10, Appl
Sequence 10, Appl
Sequence 2, Appli
Sequence 959, App
Sequence 959, App
Sequence 959, App
Sequence 2189, App
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US-09-938-842A-5203	US-10-239-676-35	US-10-240-453-43	US-10-311-455-82	US-10-239-676-144	- 1	US-10-311-455-1714	US-10-311-455-1966	US-10-311-455-1676	US-10-311-455-1290	-10-	US-10-311-455-1943	US-10-311-455-1392	US-10-027-632-128109	US-10-027-632-128109	US-10-311-455-1999	US-10-311-455-646	US-10-311-455-1763	US-10-311-455-185	US-10-240-453-313	US-10-311-455-1843		US-10-311-455-1536	US-10-311-455-2041	US-10-239-676-90	US-10-240-453-100	US-10-311-455-2045	US-10-311-455-718	US-10-312-841-2	US-10-240-452-64
5203	Sequence 35, Appl	43,	82,	144,	160,	e 1714	Sequence 1966, Ap	1676		9,									Sequence 313, App							2045	718,	e 2,	Sequence 64, Appl

ALIGNMENTS

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APPLICANT: OLSTEIN, ALAN D.

APPLICANT: FEIRTAG, JOSELLEN

TITLE OF INVENTION: BACTERIOCIN-METAL COMPLEXES IN THE DETECTION OF

TITLE OF INVENTION: PATHOGENS AND OTHER BIOLOGICAL ANALYTES

FILE REFERENCE: 7005-0003

CURRENT APPLICATION NUMBER: US/10/082,618

CURRENT FILING DATE: 2002-02-22

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PATENTIN Ver. 2.1

SEQ ID NO 8

LENGTH: 767

TYPE: DNA

ORGANISM: Streptococcus lactis

US-10-082-618-8
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US-10-082-618-8
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Publication No. US20030175207A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 767; DB 13; Length 767; Best Local Similarity 100.0%; Pred. No. 3.6e-148; Matches 767; Conservative 0; Mismatches 0; Indels 0
                             181
                                                                                 121
                                                                                                                                  121 AATAGAAACATTAACAAATCTAAAACAGTCTTAATTCTATCTTGAGAAAGTATTGGTAAT 180
                                                                                                                                                                                        61
                                                                                                                                                                                                                                       61 GAGATAGGTTTATTGAGTCTTAGACATACTTGAATGACCTAGTCTTATAACTATACTGAC 120
                                                                                                                                                                                                                                                                                                                        1 AGTTGACGAATATTTAATAATTTTAATATATCTTGATTTCCTAGTTCCTGAATAATATA 60
AATATTATTGTCGATAACGCGAGCATAATAAACCGCCTCTGATTAAATTCTGAAGTTTGTT 240
                                                                                                                                                                                        GAGATAGGTTTATTGAGTCTTAGACATACTTGAATGACCTAGTCTTATAACTATACTGAC
                                                                                 AATAGAAACATTAACAAATCTAAAACAGTCTTAATTCTATCTTGAGAAAGTATTGGTAAT 180
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; OTHER INFORMATION: chemically treated US-10-311-455-1721
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; Sequence 1721, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
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                                                                                                                                                                             NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 1721
LENGTH: 11805
                                             Matches 162;
                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                    TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ TITLE OF INVENTION: Cytosine methylation FILE REFERENCE: 5013.1014

CURRENT APPLICATION NUMBER: US/10/311,455

CURRENT FILING DATE: 2002-12-16

PRIOR APPLICATION NUMBER: PCT/EP01/07537

PRIOR FILING DATE: 2001-07-02

PRIOR APPLICATION NUMBER: DE 10032529.7

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-09-01

PRIOR FILING DATE: 2000-09-01
                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: OLEK, Alexander APPLICANT: PIEPENBROCK, Christian APPLICANT: BERLIN, Kurt
                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                      FEATURE:
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 ATTTAATTAATTTTAATTAATTATCTTGATTTTCTAGTTCCTGAATAATATAGAGATAGGTTT 71
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                                                           7.0%;
                                          Score 53.4; DB 13;
Pred. No. 0.61;
0; Mismatches 181;
                                                                                                                   genomic DNA
                                                                                                                   (Homo sapiens)
                                             Indels
                                                                         Length 11805;
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RESULT 4
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; NAME/KEY: unsure
; LOCATION: (3294164)
US-10-312-841-1
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US-10-312-841-1
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Best Local Similarity
Matches 134; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Epigenomics AG
TITLE OF INVENTION: Diagnose von bedeutenden
FILE REFERENCE: ED1/1208/WO
CURRENT APPLICATION NUMBER: US/10/312,841
CURRENT FILING DATE: 2002-12-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically
                                                                                                                                                                                                            2686756 TTTGTAGAATTTATAAAGAAATGATGGGGAAAATATATTAAAGATAGAGTGGATAAAGTA
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                                                                                                                                                        CAACCGTTTTTAGTAAGAAATACAATTTTATCTCCAAACGATAAACGGAGTTTTACTGAA
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nilarity 48.9%;
Conservative
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Application US/10311455

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FILE REFERENCE: 5013.1014

CURRENT APPLICATION NUMBER: US/10/311,455

CURRENT FILING DATE: 2002-12-16

PRIOR APPLICATION NUMBER: PCT/EP01/07537

PRIOR FILING DATE: 2001-07-02

PRIOR APPLICATION NUMBER: DE 10032529.7

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: DE 10043826.1

PRIOR APPLICATION NUMBER: DE 10043826.1

PRIOR FILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 2424

SEQ ID NO 1113

SEQ ID NO 1113
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APPLICANT: BERLIN, Kurt
ITILE OF INVENTION: Diagnosis of Diseases As;
TITLE OF INVENTION: Cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
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                                                                                                                                                                                                                                                                                                             Sequence 1200, Application US/10311455 Publication No. US20030143606A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
TITLE OF INVENTION: Cytosine methylation
                                                                                                                                                                                                                                               APPLICANT: OLEK, Alexander APPLICANT: PIEPENBROCK, Christian APPLICANT: BERLIN, Kurt
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Pred. No. 4.2;
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OTHER INFORMATION: chemically treated genomic FEATURE:
NAME/KEY: unsure
LOCATION: 11070, 11234
OTHER INFORMATION: n is a or g or c or t US-10-311-455-1200
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SEQ ID NO 1200
LENGTH: 13125
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Best Local Similarity 46.9%;
Matches 151; Conservative
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TYPE: DNA
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                                                                                                                                              CTCAACCGTTTTTAGTAAGAAATACAATTTTATCTCCAAACGATAAACGGAGTTTTACTG 660
                               TAGCTAATCCTAAACTCTATGA 742
                                                              TTGCTAAATAGCTTATAAAAATAAAGAGAGAAAAACATGATAAAAAGTTCATTTAAAG 600
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CAACCTATCAAACTCTCTATAA 1818
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Pred. No. 6.8;
                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 171;
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RESULT 6
US-10-240-485-110/c
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PRIOR APPLICATION NUMBER: PCT/EP01/03970
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR PPLICATION NUMBER: DE 10019173.8
PRIOR PRIING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR PILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
                                                                                                                                    NUMBER OF SE
SEQ ID NO 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 110,
                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/240,485
CURRENT FILING DATE: 2002-10-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: PIEPENBROCK, Christian APPLICANT: BERLIN, Kurt TITLE OF INVENTION: Diagnosis of Diseases TITLE OF INVENTION: Metastasis FILE REFERENCE: 5013.1007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: OLEK,
FEATURE: OTHER INFORMATION: chemically treated genomic
                                                             TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                             ENGTH:
                                                                                                             13125
                                                                                                                                                              SEQ ID
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o. US20030148327A1
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               DNA (Homo sapiens)
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APPLICANT: ZWIEBEL, LAURENCE J.
TITLE OF INVENTION: MOSQUITO OLFACTORY GENES, PO
TITLE OF INVENTION: USE THEREOF
FILE REFERENCE: N7841
CURRENT EPLICATION NUMBER: US/10/056,405
CURRENT FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 60/264,649
PRIOR APPLICATION NUMBER: 60/264,649
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PATENTIN VEY: 2.1
SEQ ID NO 10
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; Sequence 10, Application US/10056405
; Publication No. US20030166013A1
; GENERAL INFORMATION:
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; LOCATION: (11070, 11234)
US-10-240-485-110
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Best Local Similarity 47.0%;
Matches 149; Conservative
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Best Local Similarity 46.9%;
Matches 151; Conservative
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TYPE: DNA
ORGANISM: Anopheles gambiae
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                                                                    AATATTATTGTCGATAACGCGAGCATAATAAACGGCTCTGATTAAATTCTGAAGTTTGTT 240
                                                                                                       AATAGAAACATTAACAAATCTAAAACAGTCTTAATTCTATCTTGAGAAAGTATTGGTAAT 180
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Pred. No. 5.1;
0; Mismatches 168;
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FILE REFERENCE: N8289

CURRENT APPLICATION NUMBER: US/10/094,240

CURRENT FILING DATE: 2001-03-08

PRIOR APPLICATION NUMBER: 10/056,405

PRIOR FILING DATE: 2002-01-24

PRIOR APPLICATION NUMBER: 60/264,649

PRIOR FILING DATE: 2001-01-26

NUMBER OF SEQ ID NOS: 27

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 10
US-10-311-455-1999
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US-10-094-240-10/c
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publication No. US20030082637A1
GENERAL INFORMATION:
APPLICANT: ZWIEBEL, LAURENCE J.
TITLE OF INVENTION: ARRESTIN GENE, POLYPEPTIDE,
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Best Local Similarity 47.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Anopheles gambiae
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                                                                        2380 AATAATAATAATAA 2364
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                                                                                                                                                                                                                                                                                                                    121 AATAGAAACATTAACAAATCTAAAACAGTCTTAATTCTATCTTGAGAAAGTATTGGTAAT 180
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                                                                                                                                                                                                                                                                                                                                                                                          61 GAGATAGGTTTATTGAGTCTTAGACATACTTGAATGACCTAGTCTTATAACTATACTGAC 120
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                                                                                                                                                                                                                                                AATATTATTGTCGATAACGCGAGCATAATAAACGGCTCTGATTAAATTCTGAAGTTTGTT 240
                                                                                                       AGTACAAAAGATTTTAA 317
                                                                                                                                          AGATACAATGATTTCGTTCGAAGGAACTACAAAATTAAAATTATAAGGAGGCACTCAAAATG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 48.2; DB 15;
Pred. No. 5.1;
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Sequence 1999, Application US/10311455
Publication No. US20030143606A1
GENERAL INFORMATION:

APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, KUTC
TITLE OF INVENTION: Diagnosis of Diseases Associated with
TITLE OF INVENTION: Cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455

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CURRENT FILING.DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 1999
LENGTH: 17594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
US-10-311-455-2/c
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                                                                                                                                         APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
TITLE OF INVENTION: Cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT FILING DATE: 2002-12-16
PRIOR PELICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR FILING DATE: 2001-07-02
PRIOR FILING DATE: 2001-07-07
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 2
LENGTH: 7351
Query Match
Best Local Similarity 48.0
Matches 160; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/10311455 Publication No. US20030143606A1
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Best Local
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ORGANISM: Artificial Sequence
                                                                                                 TYPE: DNA
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                 OTHER INFORMATION: chemically treated genomic DNA
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                 48.8%;
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 Score 47.2; DB 13;
Pred. No. 9.5;
0; Mismatches 163;
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رمو 150;
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                                Length 7351;
                                                                                 (Homo sapiens)
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                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 1122
                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determi TITLE OF INVENTION: Cytosine methylation FILE REFERENCE: 5013.1014 CURRENT APPLICATION NUMBER: US/10/311,455 CURRENT FILING DATE: 2002-12-16 PRIOR APPLICATION NUMBER: PCT/EP01/07537 PRIOR PILING DATE: 2001-07-02 PRIOR PILING DATE: 2001-07-02 PRIOR APPLICATION NUMBER: DCT/EP01/07537 PRIOR APPLICATION NUMBER: DCT/EP01/07537 PRIOR APPLICATION NUMBER: DCT/EP01/07537 PRIOR APPLICATION NUMBER: DCT/EP01/07537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: PIEPENBROCK, Christian APPLICANT: BERLIN, Kurt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: OLEK, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 5452
TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                       TGACGAATATTTAATAATTATTAATATCTTGATTTTCTAGTTCCTGAATAATATATAGAG 63
                                                                                                                                                             ATTTTGTTATATTGTATATGTATTAATTTATTTTTATAGTTATAGTTATTTTTAATATTT 3866
                                                                                                                                                                                                             ATAGGTTTATTGAGTCTTAGACATACTTGAATGACCTAGTCTTATAACTATACTGACAAT 123
                                                                                                                                                                                                                                                                        ACAAAAGATTTTAACTTGGATTTGGTAT 331
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ATTATTGTCGATAACGCGAGCATAATAAACGGCTCTGATTAAATTCTGAAGTTTGTTAGA 243
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                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      6.1%;
                                                                                                                                                                                                                                                                                                                                                                                0;
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Pred. No. 9.3;
0; Mismatches 350
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; NAME/KEY: unsure
; LOCATION: (379615)
US-10-312-841-2
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US-10-312-841-2/c
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Publication No. US20030186277A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Epigenomics AG
TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
FILE REFERENCE: BO1/128/WO
CÜRRENT APPLICATION NUMBER: US/10/312,841
CÜRRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 3673778 TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                          1227150
                                                                                                 1227210
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                                                                                                                       GATAAAAAGTTCATTTAAAGCTCAACCGTTTTTAGTAAGAAATACAATTTTATCTCCAAA
TTTTTTGGAACAGTTACTACTAGCTAATCCTAAACTCTA
                                         AATAAAAAATTACTTAAACCCAAAAAATTATAACTACAATAAACCATTTATACCACTAC
                                                                                                                                                                                                         TATACCAAATAAAATACGAAAAAATTCATTTTAAAAAACTTACAATTTAATACAAACAAA
                                                                                                                                                                                                                                     TAAGCAAATAACCAAATCAAAGGATAGTATTTTGTTAGTTCAGACATGGATACTATCCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAGGTTGTAGTGAGTTAAGATTATTATTGTATATTAGTTTGGGTGATAAGAGTGAAAT 4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TACAATGATTTCGTTCGAAGGAACTACAAAATAAATTATAAGGAGGCACTCAAAATGAGT
                                                                    TTTTTATAAGTTATTTAGGGTTGCTAAATAGCTTATAAAAATAAAGAGAGGAAAAAAACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAAAGCTCAACCGTTTTTAGTAAGAAATACAATTTTATCTCCAAA 640
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                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                          chemically
                                                                                                                                                                                                                                                                          6.1%;
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                                                                                                                                                                                                                                                                            Score 47;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                         treated genomic DNA
                                                                                                                                                                                                                                                               ed. No. 1.1e+02;
Mismatches 145
                                                                                                                                                                                                                                                                                         DB 13; Length 3673778;
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US-10-311-455-959/c
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Best Local
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  FILING DATE: 2000-06-30
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; FEATURE:
; OTHER INFORMATION:
US-10-311-455-844
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases As;
TITLE OF INVENTION: Cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
                                                                                                                                                                                                                                                                   Sequence 959, Application US/10311455
Publication No. US20030143606A1
GENERAL INFORMATION:
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PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER: OF SEQ ID NOS: 2424
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TITLE OF INVENTION: Diagnosis of Diseases
TITLE OF INVENTION: cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
CURRENT FILING
                                                                                                                                                                                             APPLICANT: OLEK, Alexander APPLICANT: PIEPENBROCK, CLAPPLICANT: BERLIN, Kurt
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ORGANISM: Artificial Sequence
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20; Conservative
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Pred. No. 10;
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PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR PLING DATE: 2000-06-30
PRIOR PLING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEG ID NOS: 2424
SEQ ID NO 2189
LENGTH: 7403
TYPE: DNA
ORGANISM: Artificial Sequence
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PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 959
LENGTH: 17294
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                   Query Match
Best Local :
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Best Local Similarity 47.3%;
                                                                                                                             Matches 158;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ TITLE OF INVENTION: cytosine methylation FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: OLEK, APPLICANT: PIEPE APPLICANT: BERLI
                                                                                                                                                                                                             FEATURE: OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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    6.1%; Score 46.6;
Local Similarity 48.9%; Pred. No. 13;
hes 158; Conservative 0; Mismatches
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64 ATAGGTTTATTGAGTCTTAGACATACTTGAATGACCTAGTCTTATAACTATACTGACAAT 123
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                                     TCATTAAATTTCCTTCATTTTATTACTTTTTACATTTTATTTTATCTTTTAAAATACAC 4391
                                                                              TGACGAATATTTAATTAATATCTTGATTTTCTAGTTCCTGAATAATATAGAG
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                                                                                                                          Mismatches 159; Indels
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4150 AATAATAAAAACTACAATCACTT 4128
                                                                             4210 ААААААТАТААААААААТААТТСААТАСАААААТААТТААААТТТТААААСТТТАСТТТТА 4151
                                                                                                                                                                                                                                                                                 124
                                     298 ATGAGTACAAAAGATTTTAACTT 320
                                                                                                                AATAATATTATTGTCGATAACGCGAGCATAATAAACGGCTCTGATTAAATTCTGAAGTTT 237
                                                                                                                                                            ÄÄTÄÄTÄTTÄTTCTCTCCÄÄTTTACAAÄTÄÄAÄÄÄÄACAAAACTTAÄÄÄAAAACTAÄAAAT
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Perfect score:
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                                                                  Score
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2004 Compugen Ltd.
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AL069706 Drosophil
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BX145762 Danio rer
BX437758 BX437758
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BX422260 BX422260	BX422260	13	1201	7.1	54.8	45
) Drosophi	CNS00BO1	29	1101	7.2	55	44
-	CNSOOFUH	29	996		55	43
AL427102 clone BAG	CNS07360	29	1167		55.2	42
BX436282 BX436282	BX436282	13	1124	•	55.6	41
BX366417 BX366417	BX366417	13	986		55.6	40
BX420717 BX420717	BX420717	13	1201		55.8	39
BX414650 BX414650	BX414650	13	994	•	55.8	38
AL180950 Tetraodon	CNS024M5	29	873		55.8	37
AL106171 Drosophil	CNS0161D	29	1225	7.3	56	36
AL108811 Drosophil	CNS0182P	29	1101		56	35 5
BX415058 BX415058	BX415058		1056		56.2	34
AL106396 Drosophil	CNS0167M		1201		56.4	33
AL532464 AL532464	AL532464		1201		56.8	32
AL402900 T3 end of	CNS06KHQ		1169		56.8	31
CC238324 CH261-192	CC238324		1225		57.2	30
BX361825 BX361825	BX361825		1064		57.2	29
AL522840 AL522840	AL522840		854	•	57.2	28
AL071206 Drosophil	CNSOOFYG		1101		57.4	27
AL061936 Drosophil	CNS0021J		1101	•	57.4	26
AL103436 Drosophil	CNS013XE		893		57.4	25
AL106578 Drosophil	CNS016CO	29	1200	•	57.6	24
BX436838 BX436838	BX436838	13	985	7.5	57.8	23
AL105604 Drosophil	CNS015LM	29	1061	•	58	22
AL071865 Drosophil	CNS00DKY	29	928	•	58.2	21
B12681 F27D1-Sp6.1	B12681	28	804	•	58.4	20
BX361152 BX361152	BX361152	13	1201		58.8	19
BX377526 BX377526	BX377526	13	1098		59	18
AL104456 Drosophil	CNS014PQ	29	987		59	17
BX355654 BX355654	BX355654	13	1201		59.2	16
BX346155 BX346155	BX346155	13	960		59.2	15
AL071865 Drosophil	CNSOODKY	29	928		59.2	14
AL543368 AL543368		9	1201		59.4	.13
BX437758 BX437758	BX437758	13	1200	8.0	61	12
AL565455 AL565455		9	1201	٠	61.8	11
AL063931 Drosophil		29	1101	•	62.6	10
BX415878 BX415878	158	13	1200		63	9
6536104		ø	1201	٠	64.6	œ
BX415058 BX415058	150	13	1056		64.8	7
LS36104	104	ø	1201	8	67.2	σ
BX415878 BX415878	↦	13	1200	8.8	67.2	υ

ALIGNMENTS

RESULT 1	
CNSOORAL	
Locus	CNS00EVL 1101 bp DNA linear GSS 04-JUN-1999
DEFINITION	Drosophila melanogaster genome survey sequence T7 end of BAC:
	BACR29B23 of RPCI-98 library from Drosophila melanogaster (fruit
	fly), genomic survey sequence.
ACCESSION	AL069706
VERSION	AL069706.1 GI:4949849
KEYWORDS	GSS.
SOURCE	Drosophila melanogaster (fruit fly)
ORGANISM	Drosophila melanogaster
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
	Ephydroidea; Drosophilidae; Drosophila.
REFERENCE	1 (bases 1 to 1101)
AUTHORS	Genoscope.
TITLE	Direct Submission
JOURNAL	Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
	BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
	- Web : www.genoscope.cns.fr)
COMMENT	Determination of this BAC-end sequence was carried out as part of a
	The BDGP is constructing a physical map of the Drosophila
	melanogaster genome using these BACs. For further information
	please see http://www.fruitfly.org The BDGP Drosophila
	melanogaster BAC library was prepared by Kazutoyo Osoegawa and
	Aaron Mammoser in Pieter de Jong's laboratory in the Department of

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RESULT 2
CNS0039G/c
LOCUS
                    DEFINITION
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Drosophila melanogaster genome survey sequence TET3 end of BACR08K10 of RPCI-98 library from Drosophila melanogaster
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                                    CNS0039G
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/mol type="genomic DNA"
/mol xref="taxon:7227"
/clone="BACR29B23"
/clone="BACR29B23"
/clone=lib="RPCI-98"
/note="end : T7"
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3; Mismatches 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                        1036 WATWDTWWDKWWWWATAAKTDTAWTWWRTAWRADWAGRDRGAGKRDRDAATDADGAGRRD
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genoscope.
Direct Submission
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AL063921
AL063921.1 GI:4941778
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                                        CTCTGATGGGTTGTAACATGAAAACAGCAACTTGTCATTGTAGTATTCACGTAAGCAAAT
                                                                                                                              CAGGTGCATCACCACGCATTACAAGTATTTCGCTATGTACACCCGGTTGTAAAACAGGAG
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  {f RDRAGTAGRKWRRTWKRRWKRRDTRWDDADADDTARDDRRRRGDDGADAGKGKKTGRKRR}
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|mol_type="genomic DNA"
|/mol_type="genomic ZOA"
|/db_xref="taxon:7227"
|/clone="BACRO8K10"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Unpublished
This sequence was generated from the SP6 end of BAC 108G13. 108G13 is part of the Daniokey BAC Library created by R. Plasterk and N.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome Cambus. Hinxton. Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Actinopterygii; Neopterygii; Teleostei; Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Danio rerio
Danio rerio
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BX145762
BX145762.1 GI:27977115
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                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.sanger.ac.uk/Projects/D_rerio/
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TATTAATAATAATAATAACGTTAACAGTAGTTATAAAATTAATAATAATAATAAAT
                                                                                CATTAACAAATCTAAAACAGTCTTAATTCTATCTTGAGAAAGTATTGGTAATAATATTAT 188
                                                                                                                                                                                           AATATTTAATAATTATTAATATCTTGATTTCTAGTTCCTGAATAATATAGAGATAGG
                                                                                                                                                                      AATTATTAATAATAATAACATTAACAGTAATTAAAAATTAATAATAATAATAATAA
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                         TGTCGATAACGCGAGCATAATAAACGGCTCTGATTAAATTCTGAAGTTTGTTAGATACAA 248
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ilarity 46.9%;
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/note="vector pIndigoE
55 c 45 g
                                                                                                                                                                                                                                                                                                                                              /clone="DKEY-108G13"
                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic DNA"
/db_xref="taxon:7955"
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
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Mammalia; Eutheria; Primates;
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515
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30 c 71 g 310 t
                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9606"
/clone="CSOCAP008YB01"
/tissue_type="THYMUS"
                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                9.2%;
                                                                                                                                                                    157;
                                                                                                                                                                   Score 70.6; DB 13;
pred. No. 0.16;
7; Mismatches 357;
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Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Inbrary was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com |
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOCAPOOBCA01QP1.
Location/Qualifiers
AWWWDKRKTTTTTTTKKRRAAAATTTTTTTTTTTTTWTWAKAAAAAARAATWTTWWRAA 491
                                                         TATTGAGTCTTAGACATACTTGAATGACCTAGTCTTATAACTATACTGACAATAGAAACA 130
                                                                                                                                                                     TATTTAATAATTTTAATAATATCTTGATTTTCTAGTTCCTGAATAATATAGAGATAGGTT 70
                                                                                                                             TATWWWWDDDDAKAWADAGAATWTTTTTTWWRAGRGARKRDGTTDTRAADWWWWTWAAW 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Homo sapiens THYMUS"
/note="Vector: pcMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned the Not I and ECORV sites of the pCMVSPORT 6 vector.
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BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com |
http://fulllength.invitrogen.com/InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOCAP008BE02QP1.
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Li,W:B., Gruber,C., Jessee,J.
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/db_xref="taxon:9606"
/clone="CS0CAP008YI04"
/tissue_type="THYMUS"
                                                         organism="Homo sapiens"
                                                                                   ocation/Qualifiers
                                           _type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                             bp
Homo
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 AL536104 1201 bp mRNA line
AL536104 Homo sapiens FETAL BRAIN Homo sapiens
CSODFO22YC18 5-PRIME, mRNA sequence.
AL536104
AL536104.2 GI:31260974
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1109 TTTÄTWTWAATAAAAATTTÄTWAATÄWTWTTWÄAAWATTTTÄWTÄAATATÄTÄWWÄAAAW 1050
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TATAATAAAATAAAATATWASSVVAAAAT
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                                           CCTAAACTCTATGATGTTATGCAGAAATAT
                                                                                         CAAGTCATTGAGACTGTAAGTAAAATAAAGTTTTTTTGGAACAGTTACTACTAGCTAAT
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/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned ithe Not I and ECORV sites of the pCMVSPORT 6 vector. Library was not normalized."

10 c 85 g 447 t 170 others
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TITLE
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com
http://fulllength.invitrogen.com/ InVitroGen.Corporation 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria; Primates; Catarrhini; Ho
1 (bases 1 to 1201)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          On Feb 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Faraday Avenue Genoscope sequence ID : CSODF022BB09QP1
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP 191 91006 EVRY cedex - France
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                                                                                                                                                                       TATATAWTAWGWRTAAATAWWWWTAWAAWATWTATWTAAAAAWAWAATWWAAATATWWTT
                                                                                                                                                                                                    GTTGTAACATGAAAAACAGCAACTTGTCATTGTAGTATTCACGTAAGCAAATAACCAAAATC 478
                                                                                                                                                                                                                                                                 CACCACGCATTACAAGTATTTCGCTATGTACACCCGGTTGTAAAACAGGAGCTCTGATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMTATATTOWWTTATATAADTOTATATAAATTTWTTATWTWTTTTATTTTTWTWTATTTT 710
AGCTCAACCGTTTTTAGTAAGAAATACAATTTTATCTCCAAACGATAAACGGAGTTTTAC 658
                                                ATAWTTTATRWWATWATWTTTWWTWTTWKATTAATWATAATWWTAAWWTTTTWTATT
                                                                                                                                                                                                                                                                                                                                                                                          ATAATATTATTGTCGATAACGCGAGCATAATAAACGGCTCTGATTAAATTCTGAAGTTTG
                                                                                                            ATWATTWTTTTWTWTTTWWATWSTATWATAAAAWTAWTWTTTTTAATWTAWATAWTWT
                                                                                                                                         AAAGGATAGTATTTTGTTAGTTCAGACATGGATACTATCCTATTTTATAAGTTATTTAG
                                                                                                                                                                                                                                   TTTATWTTTTTATTATAAWTTTWTAWAWWATTWTWWWWAATWATTAGWTAWWAWWAWAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACAATAGAAACATTAACAAATCTAAAACAGTCTTAATTCTATCTTGAGAAAGTATTGGTA 178
                                                                             GGTTGCTAAATAGCTTATAAAAATAAAGAGAGAGAAAAAACATGATAAAAAAGTTCATTTAA 598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDN/
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand CDNA was digested with Not I and
cloned into the Not I and ECORV sites of the pCMVSPORT 6
vector. Library was not normalized."
a 119 c 146 g 409 t 168 others
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODF022YC18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="FETAL BRAIN"
/dev_stage="fetal"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 67.2; DE
Pred. No. 0.52;
94; Mismatches
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.52;
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3-PRIME, mRNA
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Email: seqref@genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliangelifetech.com |
http://fulllength.invitrogen.com/ InVitrogen Corporation 1600
http://fulllength.invitrogen.com/ InVitrogen Corporation 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Li,W.B., Gruber,C., Jessee,J. & Full-length cDNA libraries and Unpublished
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AAAGATTCAGGTGCATCACCACGCATTACAAGTATTTCGCTATGTACACCCGGGTTGTAAA 402 : |: |: | : | : | : | : |
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                                                                                                                                                                                                                                                                                                                                ATTGGTAATAATATTATTGTCGATAACGCGAGCATAATAAACGGCTCTGATTAAATTCTG 231
                                                                                                                                                                             AKATATAAWAAAAAAAAWAATATATAAAAAAAAAAAWAAWTTTTGWAAWATGTTTTTTK 621
                                                                                                                              AAGGAGGCACTCAAAATGAGTACAAAAGATTTTAACTTGGATTTGGTATCTGTTTCGAAG
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/db xref="taxon:966"
/clone="CSOCAPO04YG19"
/tissue type="THYMUS"
/clone_Tib="Homo sapiens THYMUS"
/clone_Tib="Homo sapiens THYMUS"
/clone="Tvector: pCMVSPORT 6; lst strand cDNA was primed // with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned int the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
Library was not normalized."
175 others
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                                                                                      al Similarity
163; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: segref@genoscope.cns.fr. Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com
http://fulllength.invitrogen.com/ InVitroGen.Corporation 1600
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1 (bases 1 to 1201)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AL536104 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone CSODF022YC18 5-PRIME, mRNA sequence.
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BP 191 91006 EVRY cedex - France
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ATWTATATATAAYMACTAWWWTAATATWAAAATHWTHTAWAAWATWTAATAATATCAAWW 1129
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                                           AAATCTAAAACAGTCTTAATTCTATCTTGAGAAAGTATTGGTAATAATATTATTGTCGAT 195
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                                                                                    8.4%;
larity 32.8%;
Conservative
                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="CSODP022YC18"
/tissue_type="FETAL BRAIN"
/tissue_type="FETAL BRAIN"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/clone_lib="Homo sapiens FETAL BRAIN"
/clone="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
/mote="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
59 a 119 C 146 g 409 t 168 others
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Pred. No. 1.3;
95; Mismatches
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                                                                                                                                                                                                                                                                                                                                 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com URL
http://fulllength.invitrogen.com/ InVitrogen.Corporation 1600
                                                                                                                                                                                                                                                                                          Faraday Avenue Genoscope sequence ID : CSOCAP008BE02QP1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                     Genoscope - Centre National de Sequencage
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
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                       428
                 /tissue_type="THYMUS"
/clone_Tib="Nomo sabjens THYMUS"
/clone_Tib="Nomo sabjens THYMUS"
/note="Vector: pcMVSPORT 6; lst strand cDNA was primed
with a NotI-oligo(dT) prImer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned i
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

170 c 85 g 447 t 170 others
                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOCAP008YI04"
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Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota, Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophila.

( bases 1 to 1101)
                                                                                                                                                                                 1101 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR08M12 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                     GCTAATCCTAAACTCTATGATGTTATGCAGAAATATAAT 761
                                                                                                                                                                                                                                                                                                                                                                                                                                           TATACTCAAGTCATTGAGACTGTAAGTAAAAATAAAGTTTTTTTGGAACAGTTACTACTA 722
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Pred. No. 2.3;
5; Mismatches 390;
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               AL565455 Homo mapiens FETAL BRAIN Homo mapiens cDNA clone CSODF005YO18 3-PRIME, mRNA mequence.
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 ALS65455
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                                                                                                                                                                                                                                                          AAAGTTCATTTAAAGCTCAACCGTTTTTAGTAAGAAATACAATTTTATCTCCAAACGATA
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                                                                                                                                                 <u>AAAARAAAAAAAAAAAAAAAATTATTTTRWAAAAATWRAAAADAKRA</u>
                                                                                                                                                                                   ATAAGTTATTTAGGGTTGCTAAATAGCTTATAAAAATAAAGAGAGGAAAAAAACATGATAA 585
                                                                                                                                                                                                                                                                                                                                                                      WWTAWAWWAATKGDGGGRARGGGGGKTTTTTKWAAAAAAAAAAWTTTTTTTAAAAATTTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGAGCTCTGATGGGTTGTAACATGAAAACAGCAACTTGTCATTGTAGTATTCACGTAAGC
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/note="end : TET3"
155 c 97 g
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/db_xref="taxon:7227"
/clone="BACR08M12"
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/mol_type="genomic DNA"
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34.9%; Pred. No. 2.7;
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Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9232.f
more information about this cluster, see
http://www.genoscope.cns.fr/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cgi-bin/cluster.cgi?seq=CSODF005BH09NF1&cluster=9232.f. Contact Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
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On Feb 16, 3
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1 (Dases 1 to 1201)

Liw B., Gruber, C., Jessee, J. and Polayes, D.
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EST.
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Location/Qualifiers
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 AAAACAGCAACTTGTCATTGTAGTATTCACGTAAGCAAATAACCAAAATCAAAGGATAGTA 489
                                                            ACAAGTATTTCGCTATGTACACCCGGTTGTAAAACAGGAGCTCTGATGGGTTGTAACATG
                                                                                            GATTTCGTTCGAAGGAACTACAAAATAAATTATAAGGAGGCACTCAAAATGAGTACAAAA 309
                                                                                                                                                                                                                   GTCGATAACGCGAGCATAATAAACGGCTCTGATTAAATTCTGAAGTTTGTTAGATACAAT
                                                                                                                                                                                                                                                                               TTATTGAGTCTTAGACATACTTGAATGACCTAGTCTTATAACTATACTGACAATAGAAAC 129
                                                                                                                                                                                                                                                                                                                                                                                                     ATTAACAAATCTAAAACAGTCTTAATTCTATCTTGAGAAAGTATTGGTAATAATATTATT
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/note="Torgan: brain; Vector: pcWVSPORT 6; lst strand cDNA
was primed with a NotI-oligo(GT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV stres of the pcWVSPORT 6
vector. Library was not normalized."
92 c 71 g 313 t 185 others
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/mol_type="mRNA"
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/dev_stage="fetal"
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/clone="CS0DF005YO18"
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Pred. No. 3.5;
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63 GATAGGTTTATTGAGTCTTAGACATACTTGAATGACCTAGTCTTATAACTATACTGACAA 122
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished
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Library was constructed by Life Technologies, a division of
Invirogen. Contact: Feng Liang Email: fliang@lifetech.com URL
http://fulllength.invitrogen.com/ Invitrogen.Corporation 1600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol type="mrNA"
/mol type="mrNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clome="CSOCAPO08YB01"
/tissue type="rHYMUS"
/tissue type="rHYMUS"
/tlosue type="rHYMUS"
/clone_Tibe="Homo sapiens THYMUS"
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                      BP 191 91006 EVRY cedex - France Email: segref@genoscope.cns.fr Email: segref@genoscope.cns.fr Technologies, a division of Liverary was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 9562.r more information about this cluster, see
                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1201)
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- Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part collaboration with the Berkeley Drosophila Genome Project (BDC The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila
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Drosophila melanogaster genome survey sequence T7 end of BAC #
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Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CS0DI001DC12QP1.
Location/Qualifiers
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/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-ollgo(dT)
/notes="ist strand cDNA was primed with a NotI-ollgo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
178 c 231 g 174 t 165 others
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/db_xref="taxon:9606"
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Pred. No. 8;
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survey sequence T7 end of BAC #
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Genoscope - Centre National de Sequencage
BRP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com |
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
                                                                                                                     Mammalia; Butheria; Primates;
1 (bases 1 to 960)
Li,W.B., Gruber,C., Jessee,J.
Full-length cDNA libraries and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the 1sogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                        BX346155
BX346155.1
                                                                                                                                                                                                                                                                                  BX346155 Homo sapiens T
                                                                                        Contact: Genoscope
                                                                                                         Unpublished
                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                        TGGTAT 331
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/note="end : T7"
70 c 84 g
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/mal_type="genomic DNA"
/db xref="taxon:7227"
/clone="BACR27A24"
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Pred. No. 9
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CELLS (JURKAT CELL LINE) COT 10-NORM
CSODJ'010YC14 5-PRIME, mRNA sequence.
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ATCCTAAACTCTATGAT 743
                                             MMAMMATMAACCACCGTCTTCTTAGAANACTGTTTTCTGGGATCTGATGTTAACCAGCC 229
                                                                                 CTCAAGTCATTGAGACTGTAAGTAAAAATAAAGTTTTTTTGGAACAGTTACTACTAGCTA
                                                                                                                                GGTGAAATGTMAAMMMAGTAGTATCTGMMGTTTGAATTAGMTGMATAAMATATATTATA
                                                                                                                                                                           CGTTTTTAGTAAGAAATACAATTTTATCTCCAAACGATAAACGGAGTTTTACTGAATATA 666
                                                                                                                                                                                                                      TAAMMMITTMÄÄÄTTÄÄTÄÄÄWAMWÄMÄMÄTMÄTÄTGTÄCMATGATTTGMMÄTGTCMÄÄ
                                                                                                                                                                                                                                                                 TAGCTTATAAAAATAAAGAGAGAAAAAAACATGATA--AAAAGTTCATTTAAAGCTCAAC
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/cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
/cell_line="JURKAT"
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10-NORMALIZED"
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Pred. No. 9.1;
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Search completed: January 12, 2004, 12:04:59 Job time : 2089 secs

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